

PATENT COOPERATION TREATY

PCT

NOTIFICATION OF ELECTION

(PCT Rule 61.2)

From the INTERNATIONAL BUREAU

To:

Commissioner
 US Department of Commerce
 United States Patent and Trademark
 Office, PCT
 2011 South Clark Place Room
 CP2/5C24
 Arlington, VA 22202
 ETATS-UNIS D'AMERIQUE
 in its capacity as elected Office

Date of mailing (day/month/year) 27 June 2001 (27.06.01)	
International application No. PCT/BE00/00077	Applicant's or agent's file reference JAN-002-PCT
International filing date (day/month/year) 03 July 2000 (03.07.00)	Priority date (day/month/year) 01 July 1999 (01.07.99)
Applicant CONTRERAS, Roland, Henri et al	

1. The designated Office is hereby notified of its election made:

☒ in the demand filed with the International Preliminary Examining Authority on:
 22 January 2001 (22.01.01)

☐ in a notice effecting later election filed with the International Bureau on:

2. The election ☒ was

☐ was not

made before the expiration of 19 months
 Rule 32.2(b).

2 applies, within the time limit under

The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland Facsimile No.: (41-22) 740.14.35	Authorized officer Pascal Piriou Telephone No.: (41-22) 338.83.38
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(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
11 January 2001 (11.01.2001)

PCT

(10) International Publication Number
WO 01/02550 A2

(51) International Patent Classification⁷: C12N 15/00

Beerse (BE). REEKMANS, Rieka, Josephina [BE/BE];
Wijnbergstraat 190, B-8560 Wevelgem (BE).

(21) International Application Number: PCT/BE00/00077

(22) International Filing Date: 3 July 2000 (03.07.2000)

(74) Agent: COIGNEZ, Koen; De Clercq, Brants & Partners
cv, E. Gevaertdreef 10 a, B-9830 Sint-Martens-Latem (BE).

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(71) Applicant (*for all designated States except US*):
JANSSEN PHARMACEUTICA N.V. [BE/BE]; Turnhoutseweg 30, B-2340 Beerse (BE).

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): CONTRERAS, Roland, Henri [BE/BE]; Molenstraat 53, B-9820 Schelderode (BE). DE BACKER, Marianne, Denise [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). LUYTEN, Walter, Herman, Maria, Louis [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). MALCORPS, Isabelle, Karin, Luc [BE/BE]; Begijnenstraat 18, B-2980 Zoersel (BE). NELISSEN, Bart, Jozef, Maria [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340

Published:

— Without international search report and to be republished upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

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(51) International Patent Classification⁷: **C12Q 1/68**,
C12N 15/81, A61P 31/04, 31/10, C07K 14/395, 14/40,
16/14

Beerse (BE). REEKMANS, Rieka, Josephina [BE/BE];
Wijnbergstraat 190, B-8560 Wevelgem (BE).

(21) International Application Number: PCT/BE00/00077

(74) Agent: COIGNEZ, Koen; De Clercq, Brants [entity:amp]
Partners cv, E. Gevaertdreef 10 a, B-9830 Sint-Martens-
Latem (BE).

(22) International Filing Date: 3 July 2000 (03.07.2000)

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE,
DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,
ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(71) Applicant (*for all designated States except US*):
JANSSEN PHARMACEUTICA N.V. [BE/BE]; Turn-
houtseweg 30, B-2340 Beerse (BE).

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): CONTRERAS,
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Schelderode (BE). DE BACKER, Marianne, Denise
[BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg
30, B-2340 Beerse (BE). LUYTEN, Walter, Herman,
Maria, Louis [BE/BE]; Janssen Pharmaceutica N.V.,
Turnhoutseweg 30, B-2340 Beerse (BE). MALCORPS,
Isabelle, Karin, Luc [BE/BE]; Begijnenstraat 18, B-2980
Zoersel (BE). NELISSEN, Bart, Jozef, Maria [BE/BE];
Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340

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— with international search report

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 01/02550 A3

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INTERNATIONAL SEARCH REPORT

International Application No

PC 1/BE 00/00077

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68 C12N15/81 A61P31/04 A61P31/10 C07K14/395
C07K14/40 C07K16/14

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE TREMBL [Online] EMBL database Heidelberg ac: p89096, 1 May 1997 (1997-05-01) KOBAYASHI O. ET AL.: "The region of Flo1 protein responsible for sugar recognition." XP002135238 abstract	1-16,34, 38,39, 44-55
X	--- DATABASE SWISS PROT [Online] ac: p39561, 1 February 1995 (1995-02-01) BUSSEY H. ET AL.: "gene: YAR061W" XP002135239 hypotetical 7.6 kD protein in FL01-PH011 intergenic region. abstract --- -/--	1-16,34, 38,39, 44-55

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *G* document member of the same patent family

Date of the actual completion of the international search

7 June 2001

Date of mailing of the international search report

28.8.01

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel: (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Panzica, G

INTERNATIONAL SEARCH REPORT

International Application No

PCT/BE 00/00077

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	LIGR M. ET AL.: "Mammal Bax triggers apoptotic changes in Yeast" FEBS LETTERS, vol. 438, 1998, page 61-65 XP000857722 AMSTERDAM NL the whole document	1-16,34, 38,39, 44-55
X	US 5 882 874 A (FISHER PAUL B) 16 March 1999 (1999-03-16) the whole document	1-16,34, 38,39, 44-55
X	US 5 700 644 A (ARIAZI ERIC A ET AL) 23 December 1997 (1997-12-23) the whole document	1-16,34, 38,39, 44-55
Y	RESEARCH GENETICS: HTTP://WWW.APPS.RESGEN.COM/YEAST ORF/YEAST _ORF_LOC_MAIN.HTLM,1998, XP002134776 the whole document	1-16,34, 38,39, 44-55
Y	WO 95 28497 A (JOLLA CANCER RES FOUND) 26 October 1995 (1995-10-26) abstract page 21, line 12 - line 31 example 1	1-16,34, 38,39, 44-55
Y	GB 2 326 413 A (NOVARTIS AG) 23 December 1998 (1998-12-23) abstract examples 1-9	1-16,34, 38,39, 44-55
X	MADEO FRANK ET AL: "A yeast mutant showing diagnostic markers of early and late apoptosis." JOURNAL OF CELL BIOLOGY, vol. 139, no. 3, 3 November 1997 (1997-11-03), pages 729-734, XP002168669 ISSN: 0021-9525 abstract	1-6,34, 38,39, 44-55
X	MARZO ISABEL ET AL: "Bax and adenine nucleotide translocator cooperate in the mitochondrial control of apoptosis." SCIENCE (WASHINGTON D C), vol. 281, no. 5385, 1998, pages 2027-2031, XP000982449 ISSN: 0036-8075 abstract	1-16,34, 38,39, 44-55

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/BE 00/00077

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>MATSUYAMA S ET AL: "THE MITOCHONDRIAL F₀F₁-ATPASE PROTON PUMP IS REQUIRED FOR FUNCTION OF THE PROAPOPTOTIC PROTEIN BAX IN YEAST AND MAMMALIAN CELLS" MOLECULAR CELL,CAMBRIDGE, MA,US, vol. 1, February 1998 (1998-02), pages 327-336, XP000987219 ISSN: 1097-2765 the whole document</p> <p style="text-align: center;">---</p>	<p>1-16,34, 38,39, 44-55</p>
A	<p>XU QUNLI ET AL: "Methods of assaying Bcl-2 and Bax family proteins in yeast." METHODS (ORLANDO), vol. 17, no. 4, April 1999 (1999-04), pages 292-304, XP002168670 ISSN: 1046-2023 the whole document</p> <p style="text-align: center;">---</p>	<p>1-16,34, 38,39, 44-55</p>
A	<p>SUN J ET AL: "SCREENING FOR BCL-2 HOMOLOGUES IN ASPERGILLUS NIDULANS" FASEB JOURNAL,FED. OF AMERICAN SOC. FOR EXPERIMENTAL BIOLOGY, BETHESDA, MD,US, vol. 11, 1997, page A425 XP000982451 ISSN: 0892-6638 abstract</p> <p style="text-align: center;">---</p>	<p>1-16,34, 38,39, 44-55</p>
A	<p>TAO W ET AL: "IDENTIFICATION OF YEAST PROTEINS THAT BIND SPECIFICALLY TO BCL-2" FASEB JOURNAL,FED. OF AMERICAN SOC. FOR EXPERIMENTAL BIOLOGY, BETHESDA, MD,US, vol. 11, 1997, page A1240 XP000982452 ISSN: 0892-6638 the whole document</p> <p style="text-align: center;">---</p>	<p>1-16,34, 38,39, 44-55</p>
A	<p>TAO W ET AL: "MODULATION OF CELL DEATH IN YEAST BY THE BCL-2 FAMILY OF PROTEINS" JOURNAL OF BIOLOGICAL CHEMISTRY,AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD,US, vol. 272, no. 24, 13 June 1997 (1997-06-13), pages 15547-15552, XP000982450 ISSN: 0021-9258 the whole document</p> <p style="text-align: center;">-----</p>	<p>1-16,34, 38,39, 44-55</p>

INTERNATIONAL SEARCH REPORT

International application No.
PCT/BE 00/00077

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-16,34,38,39,44-55 (in part)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-16, 34, 38, 39, 44-55 (in part)

Invention 1:

Nucleic acid as set forth in Seq.Id.No.1 and protein sequence as set forth in Seq.Id.No.2 of the sequence listing, their methods of production and uses in medical preparations against disorders caused by Fungi or Yeast.

2. Claims: 1-55 in part

Inventions 2 to 228:

Same as for invention 1 but in relation to each group of nucleic acid sequence and its relative aminoacid sequence:

Invention 2: Seq.Id.Nos. 3 and 4,

...

Invention 228: Seq.d.Nos. 455 and 456.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/BE 00/00077

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
US 5882874	A	16-03-1999	AU	2881799 A	15-09-1999
US 5700644	A	23-12-1997	NONE		
WO 9528497	A	26-10-1995	AU	2290195 A	10-11-1995
			EP	0759090 A	26-02-1997
			US	5702897 A	30-12-1997
GB 2326413	A	23-12-1998	NONE		

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference -----	FOR FURTHER ACTION See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)	
International application No. PCT/BE00/00077	International filing date (day/month/year) 03/07/2000	Priority date (day/month/year) 01/07/1999
International Patent Classification (IPC) or national classification and IPC C12N15/00		
Applicant JANSSEN PHARMACEUTICA N.V. et al.		

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.



2. This REPORT consists of a total of 10 sheets, including this cover sheet.

- ☒ This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of 3 sheets.

3. This report contains indications relating to the following items:

- I ☒ Basis of the report
- II ☐ Priority
- III ☒ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
- IV ☒ Lack of unity of invention
- V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
- VI ☐ Certain documents cited
- VII ☒ Certain defects in the international application
- VIII ☒ Certain observations on the international application

Date of submission of the demand 22/01/2001	Date of completion of this report 25.09.2001
Name and mailing address of the international preliminary examining authority:  European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465	Authorized officer Nichogiannopoulou, A Telephone No. +49 89 2399 8054 

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/BE00/00077

I. Basis of the report

1. With regard to the **elements** of the international application (*Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17)*):

Description, pages:

1-41 as originally filed

Claims, No.:

1-55 as originally filed

Drawings, sheets:

1/161-21/161,23/161-27/161, as originally filed
29/161-56/161,
58/161-161/161

22/161,28/161, as received on 23/11/2000 with letter of 22/11/2000
57/161

Sequence listing part of the description, pages:

1-570, filed with the letter of 24.10.2000

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☐ contained in the international application in written form.
- ☐ filed together with the international application in computer readable form.
- ☒ furnished subsequently to this Authority in written form.
- ☒ furnished subsequently to this Authority in computer readable form.
- ☒ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

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EXAMINATION REPORT**

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- ☒ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
☐ the claims, Nos.:
☐ the drawings, sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

6. Additional observations, if necessary:
see separate sheet

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

1. The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

- ☐ the entire international application.
☒ claims Nos. 1-16, 34, 38, 39, 44, 45, all partially, 17-33, 35-37, 40-43 all completely.

because:

- ☒ the said international application, or the said claims Nos. 44, 45 relate to the following subject matter which does not require an international preliminary examination (*specify*):
see separate sheet

- ☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):

- ☒ the claims, or said claims Nos. 11-14, 16, 40-43 are so inadequately supported by the description that no meaningful opinion could be formed.

- ☒ no international search report has been established for the said claims Nos. 1-16, 34, 38, 39, 44-55 all partially, 17-33, 35-37, 40-43 all completely.

2. A meaningful international preliminary examination cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

- ☐ the written form has not been furnished or does not comply with the standard.



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- ☐ the computer readable form has not been furnished or does not comply with the standard.

IV. Lack of unity of invention

1. In response to the invitation to restrict or pay additional fees the applicant has:

- ☐ restricted the claims.
- ☐ paid additional fees.
- ☐ paid additional fees under protest.
- ☐ neither restricted nor paid additional fees.

2. ☐ This Authority found that the requirement of unity of invention is not complied and chose, according to Rule 68.1, not to invite the applicant to restrict or pay additional fees.

3. This Authority considers that the requirement of unity of invention in accordance with Rules 13.1, 13.2 and 13.3 is

- ☐ complied with.
- ☒ not complied with for the following reasons:
see separate sheet

4. Consequently, the following parts of the international application were the subject of international preliminary examination in establishing this report:

- ☐ all parts.
- ☒ the parts relating to claims Nos. 1-16, 34, 38, 39, 44-55.

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Yes:	Claims
	No:	Claims 1-16, 34, 38, 39, 44-55
Inventive step (IS)	Yes:	Claims
	No:	Claims 1-16, 34, 38, 39, 44-55
Industrial applicability (IA)	Yes:	Claims
	No:	Claims 1-16, 34, 38, 39, 44-55

2. Citations and explanations
see separate sheet

VII. Certain defects in the international application

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/BE00/00077

The following defects in the form or contents of the international application have been noted:
see separate sheet

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:
see separate sheet

Re Item I

Basis of the report

1. The amendments to the drawings filed with the letter of 22.11.2000 are formally allowable under Article 34(2)(b) PCT because they are the corrections of obvious errors under Rule 91.1 and do not introduce subject-matter extending beyond the content of the application as filed.

Re Item III

Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

1. No meaningful examination could be performed for claims 1-16, 34, 38, 39, 44-55 all partially and 17-33, 35-37, 40-43 all completely, for the following reasons:
 - 1.1. Rule 66. 1.(e) (PCT):

No complete international search report has been established for claims 1-16, 34, 38, 39, 44-55 all partially and 17-33, 35-37, 40-43 (see Form PCT/ISA/210 issued on 28/08/2001). Accordingly, said claims need not be the subject of international preliminary examination.
 - 1.2. Articles 5 and 6 PCT:

Claims 11-14, 16 and 40-43 do not comply with the requirements of Articles 5 and 6 (PCT). Said claims relate to compounds identifiable by the claimed methods without giving a true technical characterisation of such compounds. Moreover no such compounds are disclosed in the present application. In consequence the scope of said claims is ambiguous and vague and their subject-matter is neither sufficiently disclosed nor supported. These deficiencies render a meaningful examination of the claimed subject-matter impossible.

2. Claims 44 and 45 -as far as they concern in vivo methods- relate to subject-matter considered by this Authority to be covered by the provisions of Rule 67.1(iv) PCT. Consequently, no opinion will be formulated with respect to the industrial applicability of the subject-matter of these claims (Article 34(4)(a)(i) PCT).

Re Item IV**Lack of unity of invention**

1. The present application lacks unity as required by Article 3(4)(iii) PCT and Rule 13 PCT. Rule 13.1 PCT states that for unity of invention to be present, all subject-matter should be linked by a single general inventive concept. Each of the 228 groups of inventions listed on Form PCT/ISA/206 issued on 28.06.2001 constitutes a separate, distinct invention for the following reason. The common concept linking these 228 groups is that they are all allegedly involved in a Bax-induced apoptotic pathway in yeast. Bax induction of apoptotic pathways in yeast has already been known from the prior art. **D3** teaches that Bax induces an apoptotic cascade in yeast and discloses genes involved in a pathway leading to apoptosis and their use for killing yeast. Since no other "special" technical feature (Rule 13.2 PCT) could be identified to provide a linking concept between the four groups, each must be considered as a separate invention.

N.B. The use of the term "invention" here in no way implies recognition of an inventive step for the subject-matter of any group.

Re Item V

Reasoned statement under Article 35(2) with regard to novelty, inventive step or

industrial applicability; citations and explanations supporting such statement

1. Reference is made to the following documents:

- D1: DATABASE TREMBL [Online] EMBL database Heidelberg ac: p89096, 1 May 1997 (1997-05-01) KOBAYASHI O. ET AL.: 'The region of Flo1 protein responsible for sugar recognition.' XP002135238
- D2: DATABASE SWISS PROT [Online] ac: p39561, 1 February 1995 (1995-02-01) BUSSEY H. ET AL.: 'gene: YAR061W' XP002135239
- D3: LIGR M. ET AL.: 'Mammal Bax triggers apoptotic changes in Yeast' FEBS LETTERS, vol. 438, 1998, page 61-65 XP000857722 AMSTERDAM NL

2. **Novelty** (Article 33(2) PCT)

The present application discloses sequences involved in the molecular pathways leading to apoptosis in yeast. The claimed sequences were obtained by differential display screening of Bax induced mRNAs on arrays of yeast ORFs. The use of such sequences in pharmacy is alleged. There is no indication of a function of the claimed cDNAs.

D1 and **D2** are database entries that are identical to SEQ ID Nos:1 and 2 of the present application. **D3** discloses that Bax induces apoptotic pathways in yeast. **D1-D3** are thus detrimental to the novelty and inventive step of claims 1-16, 34, 38, 39 and 44-45.

3. **Inventive step** (Article 33(3) PCT)

Due to the fact that no function has been established for the claimed sequences, these do not appear to be associated with any known technical effect. Accordingly, the only underlying technical problem that can be recognised is the provision of sequences somehow associated with the apoptotic pathway in yeast. To establish inventive activity,

the provision of a sequence must be justified by the technical purpose, i.e. by a

hitherto unknown or unexpected technical effect, caused by those technical features which distinguish the claimed molecules from numerous other ones. Due to the absence of any disclosed function or technical effect, the provision of the present sequences amounts to nothing more than an arbitrary selection. Consequently, the claimed molecules as well as compositions, vectors, host cells kits and methods relating to them (claims 1-16, 34, 38, 39 and 44-45) are considered to lack an inventive step, pursuant to Article 33(3) PCT.

4. Industrial applicability (Article 33(4) PCT)

In so far as the present specification is completely silent with regard to the function of the claimed sequences, the possible fields of application for the claimed protein and polynucleotides suggested in the specification are merely speculative. Thus it is questionable whether the claimed subject-matter actually meets the requirements set forth in Article 33(4) PCT.

Re Item VII

Certain defects in the international application

1. Contrary to the requirements of Rule 5.1(ii) PCT, documents D1-D3 are not identified in the description and the relevant background art disclosed therein is not briefly discussed.

Re Item VIII

Certain observations on the international application

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT - SEPARATE SHEET**

International application No. PCT/BE00/00077

1. The claimed use of the disclosed sequences for the preparation of a medicament for treating diseases associated with yeast or fungi is neither disclosed in nor supported by the application as filed. Such use is purely hypothetical and amounts to little more than an unsubstantiated desideratum. Accordingly, claims 1-4, 15, 44-48 do not fulfill the requirements of Articles 5 and 6 EPC.
2. In this context it should also be noted that even the relation of the disclosed sequences with apoptosis is purely hypothetical: Bax-induced or Bax-regulated expression or over-expression of genes and apoptotic pathways are related but not overlapping concepts. There is no evidence that every Bax regulated sequence is involved in apoptosis, even if such involvement were sufficient to justify speculations on a medical use.
3. Furthermore, present claims 1 and 2 do not satisfy the provisions of Article 6 PCT in that the term "functional equivalents" and "functional fragment" is unclear. A functional equivalent of a sequence involved in an apoptotic pathway in yeast is **any** sequence somehow involved in an apoptotic pathway in yeast. Claims to such an equivalent would have to be additionally defined in terms of its sequence for the purposes of Article 6 PCT.

CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

Invasive fungal infections (e.g. *Candida* spp, *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. To

survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has been assumed that such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a similar process of cell survival also operates in single-celled eukaryotes.

It has been found that expression of the mammalian *Bax* gene triggers cell death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997). However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes.

It is an aim of the present invention to provide nucleic acid as well as polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases associated with yeast or fungi.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast or fungi infections. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds.

It is also an aim of the invention to provide a method of preventing infection with yeast or fungi.

It is also an aim of the invention to provide probes and primers derived from the nucleic acid sequences of the invention.

All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 2, genes showing a difference of a factor 5 or more in expression as a result of *Bax*-induced cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a *Bax*-expressing strain, while other genes show an upregulated expression (Table 1). Example 3 describes a further experiment wherein the results of differential expression were analysed using the Pathways™ software and differentially expressed nucleic acid sequence were identified.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more

- preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using
5 BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide
10 or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to
15 determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine
20 identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15,
25 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
30 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473 .

The invention also relates to nucleic acid sequences from *Candida albicans*, as represented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303,
35 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

5 The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

10 The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

15 The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

20 The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

35 According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides.

Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

(c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483; and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f).
- According to a more specific embodiment, these nucleic acid sequences are derived from *Saccharomyces cerevisiae*, *Candida albicans* or *Aspergillus fumigatus*.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook et al., 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

5 The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given, or the antisense version thereof.

The invention also relates to mRNA, DNA or cDNA versions of the nucleic acid molecules of the invention.

10 The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

15 The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically
20 with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under
25 hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto
30 the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR
35 cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be

cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined
5 herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzym
10 labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a
15 suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be
20 a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of th
25 invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

30 Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and
35 fungi with reductions of associated illnesses or diseases s.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2,
5 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,
50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126,
128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158,
160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
10 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,
224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286,
288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350,
15 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382,
384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414,
416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446,
448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478,
480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of
20 said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar,
preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid
sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28,
25 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,
74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,
114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144,
146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,
178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
30 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240,
242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304,
306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336,
338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368,
35 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400,
402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids,

amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

The term "cells" as used above relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein

differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: on one of the binding partners, compound or polypeptide is labelled and interaction of both is measured. Most of these tests comprise the following steps:

incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence

according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose

will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling on of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nev rtheless, m dium or low throughput systems can b used to confirm results obtained by the high throughput assays or in cases wher none of the binding partners ar labeled. Other techniques which can be used to study interactions ar : overlay, ligand blotting, band-shift, co-

immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo model systems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

The compounds of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections,

for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
5 and *Sporothrix schenckii* infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

10 A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids or polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of
15 said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

20 Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi
25 selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394,
30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or
35 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,

306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452
5 454, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 75% or 80% identical, more preferably more than 85%, 90%
or 95% identical and most preferably more than 97% identical to any of the amino
acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302,
10 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342,
344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376,
380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416,
418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450,
452, 454, 476, 478, 480, 482, or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as
a medicament.

Also encompassed within the present invention are antibodies, monoclonal or
polyclonal, capable of specifically binding to one or more epitopes of the proteins of the
20 invention. The term "specific binding" implies that there is substantially no cross-
reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to
techniques which are known to those skilled in the art. Monoclonal antibodies may be
prepared using conventional hybridoma technology as described by Kohler and
25 Milstein (1979). Polyclonal antibodies may also be prepared using conventional
technology well known to those skilled in the art, and which comprises inoculating a
host animal, such as a mouse, with a protein or epitope according to the invention and
recovering the immune serum. The present invention also includes fragments of whole
antibodies which maintain their binding activity, such as for example, Fv, F(ab') and
30 F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of
detecting the presence of a polypeptide according to the invention, which method
comprises reacting the antibody with a sample and identifying any protein bound to
said antibody. A kit may also be provided for performing said method which compris
35 an antibody according to the invention and means for reacting the antibody with said
sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to,
5 *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium* spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

10 According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic
15 acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art
20 (Sambrook et al., 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides
25 of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

The invention further relates to the compounds identifiable according to the above-described method and its use as a medicament.

The invention further relates to a method for preparing a pharmaceutical
30 composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate
35 due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal

benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

5 The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

10 According to another embodiment, the invention relates to the use of a nucleic acid molecule or a polypeptide described in the invention or human homologues thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

15 The invention also relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

20 The invention also relates to a vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically acceptable carrier.

25 The invention also relates to the use of an antibody of the invention capable of binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

30 According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention. Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

35 According to another embodiment the invention relates to a nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences described in the invention.

The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

5 The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the invention.

10 The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

- Figur 1.** *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)
- Figure 2.** *Candida albicans* sequences (SEQ ID Nos 285 to 456).
- 5 **Figure 3.** Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
- 10 The spots represent the genome wide expression profile without (A) and with (B) *Bax* modulated expression (Example 2).
- Figure 4.** Results from a second experiment analogous and analysed as described in the examples section (Example 3).
- 15 **Table 1.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a
- 20 downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to *Bax* expression in *S. cerevisiae*. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0,21, respectively.
- 25 **Table 2.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

EXAMPLES**Example 1. Differential gene expression analysis upon Bax-induced cell death****Materials and media**

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTyLMuBax, after linearisation in the Ty δ element (Zhu, 1986).

Cloning of mouse BAX cDNA

Mouse Bax cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' and
5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

Plasmid constructions

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Clal* and *BglII*. A *BamHI-HindIII* GAL1 promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* FLP terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse Bax cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as p5CTyGALmBax with accession number 3871 under restricted use.

Gen Filters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

5 The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

10 Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

15 The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains
20 the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

25

Results**Induction of Bax-expression in yeast cells**

30 *S. cerevisiae* cells (strain INVSc1) were transformed with the expression plasmid YIpUTyLMuBax or the parental plasmid YIpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

The Ty δ element of both plasmids allowed a stable multi-copy integration in the genome of the yeast cell. Southern analysis of the cells containing YIpUTyLMuBax
35 revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty elements.

The yeast cells containing YlpUTyLMuBax and the yeast cells containing YlpUTyL were grown overnight in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YlpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YlpUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

RNA isolation

Total RNA was isolated using RNAPure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 · 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

First strand cDNA synthesis in the presence of α-³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL yeast cells and incorporation of α-³³P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

- 6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
- 1 µl 0,1 M DTT
- 1 µl RNas Block (40 units/µl) (Stratagene)
- 1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
- 1,5 µl SuperScript™ Revers Transcriptase (200 units/µl) (GIBCO-BRL)
- 10 µl α-³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 3 or 5 10^8 cpm/ μ g for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α - 33 P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 or 10 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (0,5 or 1 μ g/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

Exempl 2. Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.
2. The frequency in terms of percentage.
3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

Subsequently, the results of the two experiments (hybridization with cDNA from YIpUTyL containing INVSc1 cells and hybridization with cDNA from YIpUTyLMuBax containing INVSc1 cells) were integrated by determination of a second range of statistical functions:

1. The average of the values of the two experiments for each spot on the filter.
2. The standard deviation on this average. This is a measure for the distribution of the values around this average.
3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately gave the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidate gene. (Table 1).

Requantification of these candidates confirmed their selection.

When the expression pattern of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3 %) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1. The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

Example 3 . Quantification of Hybridisation Signals using the Pathways™ software

Quantification of the hybridisation signals was done using the Pathways™ Software (Research Genetics) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 2.

Surprisingly, using this Software package for analysing the results in this example and when compared to the results of example 2, some additional genes were found which expression are up-or down-regulated upon *Bax* expression in *S. cerevisiae*.

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in *Candida albicans*

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minnesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

Exempl 5 . Screening f r comp unds modulating expression of p lypeptides involved in induction of cell death of *C. albicans*

5 The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in th macromolecule catalyzing that step and/or less potent macromolecule, as compared to
10 the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally
15 sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whos growth is affected by a test compound is potentially the site of action of the test
20 compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-
25 sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

30 **Example 6. Assay for High Throughput screening for drugs**

35 35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plat into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with $20\text{ }\mu\text{g/ml}$ uridine. A single colony is scooped
5 up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml.
10 Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (± 0.04) is reached.

200 μl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

15 Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Tabl 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103

YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211

YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Table 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which
5 nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

- 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,

- 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; and
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),
- for the preparation of a medicament for treating diseases associated with yeast or fungi.

2. Use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

25

3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

30

4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.

35

5. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

5 6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 10 (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- 15 (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

25 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 30 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 35 (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is

indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- 5 (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 10 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

15

- (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
- (b) detecting the complex formed between the compound to be tested and said polypeptide,
- 20 (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound being tested.
- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.
- 25

9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
- 30 (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.
- 5 11. A compound identifiable according to the method of any of claims 6 to 9.
12. A compound according to claim 11 for use as a medicament.
- 10 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.
14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.
- 15 15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
- 20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
25 and *Sporothrix schenckii*.
17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- 30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
35 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 10 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 15 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 20 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 25 (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- 30 (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 35 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).

5 18. A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.

 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.

10

 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA

 21. A nucleic acid sequence according to any of claims 17 to 19 which is
15 DNA.

 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.

20 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.

 24. An isolated protein which is involved in a pathway for programmed cell
25 death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and
35 most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348,
352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384,
386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424,
426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476,
5 478, 480, 482 or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 80% identical, more preferably more than 90% identical
and most preferably more than 97% identical to any of the amino acid
sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,
10 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,
454, 476, 478, 480, 482 or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c)

25. An expression vector comprising a nucleic acid sequence according to
any of claims 17 to 23 .

20 26. An expression vector according to claim 25 which comprises an
inducible promoter.

27. An expression vector according to claim 25 or 26 which comprises a
sequence encoding a reporter molecule.

25 28. A host cell transformed, transfected or infected with the vector of any of
claims 25 to 27.

29. A nucleic acid molecule according to any of claims 17 to 23 for use as a
30 medicament.

30. A polypeptide according to claim 24 for use as a medicament.

31. An antibody capable of specifically binding to a polypeptide according to
35 claim 24.

32. An antibody according to claim 31 for use as a medicament.

33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.

5

34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.

10

35. Use of an antibody according to claim 34 where the fungus is *Candida albicans*.

15

36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively hybridises with any of said nucleic acid molecules.

20

37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.

25

38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

30

39. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

35

40. A compound identifiable according to the method of claim 39.

41. A compound according to claim 40 for use as a medicament.

42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising
5 admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain
10 disorders.

44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
15

45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
20
25

47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.
30

48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
35

49. An expression vector comprising a human homologue of a nucleic acid sequence as defined in claim 1.

50. An expression vector according to claim 49 which comprises an inducible promoter.

5

51. An expression vector according to claim 49 or 50 which comprises a sequence encoding a reporter molecule.

52. A host cell transformed, transfected or infected with the vector of any of claims 49 to 51.

10

53. A nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences as defined in claim 1.

15

54. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 53.

55. A polypeptide encoded by a nucleic acid molecule according to claim 53.

20

FIG. 1:

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGGAGTTCCTCAAGACTTATACTT
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTTCGTTACAACCTGCTGCAGGACTCTT
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT
TAATTTTTTTTCTTGAACCTTGTTGAGTCGTAATAAATCGTTTCTGGGAAGTGGAAGGTAAT
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAAGTGTGTAGG
GACGTTTCGATACCAAAATTTCTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTTATTTTTGGCACTCTTCACCTACC
TGGCCAGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCCGAGGA
AAAATGGGATGAATGTCAACTTTTATAAATACTCATTACTGGATTCAACAACGTATTCCCT
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFLALFTYLATSNVVSSTQACLPGVPRKNGMNVNFYKYSLLDSTTYSYPQYMTS
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA
AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTATTCAAGATTATTGGTTTTTC
CTAACCGCCGCGCGCGCAGGTACCCCGCGCATCTCTTCTCTCGAAGAAAGCGGAAAAA
ACAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTTAACATTTAGAAAAAATTCG
AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCTTGCGGGCTTTTTCTCAGTTTCG
TGGGCTAGTACATTTTACCTAGTATGCTGGGAACCTTTTTTCCGTATTCTATTCTATTCC
TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTTAACTGTC
ATAGACGCATTTTGTATTATTACAAATTAAGAATCAAATATAATATGTGCAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTTGTCTAGTGCAGGAAGTATGGACTCCAAGATCA
GAGGTGGGTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTGGCTCCT
CTGAAGTTAGCCTACAGACCAAGCTAACCCAGGAATATTACTTTAAACATTTCCATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG
GTATCGGTTTTCATTACCATTAACCTGTAATCCAGAGGACCAAGCTGACATGGTGAAGAG
TCAAGAACTATGAAAATGGGTTTATTAACAACCTTATAGTGATTTCTCCAACCTACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTTGCAGGCTTCCCTGTCACGGCAG
ATGGAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG
AGGACAACCTCTTTACTCGTTCAGGATGTCATGACCAAAAACCTGTTACCGGCGCACAAG
GTATCACATTATCAGAAGGTAACGAAATCTTAAAGAAAATCAAAAAGGGTAGGCTACTGG
TTGTTGATGAAAAGGGTAACTTAGTTCTATGCTTTCCCGAACTGATTTAATGAAAAATC
AGAAGTACCCATTAGCGTCCAAATCTGCCAACCAAGCAACTGTTATGGGGTGGCTTCTA
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG
TCGTCATATTGGATTCCCTCTCAAGGTAACCTCTATTTTCCAATTGAACATGATCAAATGGA
TTAAAGAACTTTCCAGATTGGAATCATTGCTGGTAACGTTGTCACCAAGGAACAAG
CTGCCAATTTGATTGCTGCCGCTGCGGACGGTTTGAGAATTGGTATGGGAAGTGGCTCTA
TTTGTATTACCCAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG
TGTGTGAATTTGCTAACCAATTCGGTGTTCATGTATGGCTGATGGTGGTGTTCAAAAAC
ATTGGTCATATTATTACCAAGCTTTGGCTCTTGGTCTTCTACTGTATGATGGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGIGFIHNCPTPEDQADMVRRVKNYENG
FINNPVIVISPTTTVGEAKSMKEKYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVVDEKGNLVSMLSRTDLMKNQKYPLAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGRLDVILDSSQGNISIFQLNMIKWIKYETFPD
LEIIAGNVVTKEQAANLIAAGADGLRIGMGTGSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWSYYYQSFSGSWFFYCYDGWYVGRYYRITR

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)
GGGAGAAGCTTATCTTACTGTAGAGAAGAAATGGGATTGCGTTACTCCATATATATTGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTTCCACTCTC
AGCATCGATCGCAAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCCAGTTCCCTCCAGATTATTTCTAGAGATTATAGGGGTAGGACCGGAAGTCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTCGAGCAACGAAGAATGTTGA
CTGGCGACTACTTAGTCTGTGATATTCTTTGTCATTGGTGCAAGAGGAACGTAGGTTGGA
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTTGTAAATGTACTTGATGTCTTCCTTTGTCTGCTATCTAGCACCTCTCGT
CTTTTAGTGCTTTTTTAGCGTATGATTCTTTTAAAGAATCTGGTCTTTCCTTCTATTT
TGATTGGGTATATTTCTATTTCGTGTTTCATTACTGGTCTGGGTTAATTGGGTTTTGGTTT
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTCATTGTGGTATTTTATCTTATCGATT
ATACTTTTTTTTATTCAAAGAAAATTAACAGATAATCTCTTATGAGCCTAGCTACTTTG
TTTTTTCTTACAGGGCCATTGACTTATGCCCTGAACGAGTCTTACTTTACTTTTTTTGTA
TTTTCAATAATGTCGTGTTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)
MILFKNLVFLPSILIGYISIRVSLVWVNWVLVWSSCFQVAFIFSLWYFILSIYTFYFSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVVFPM

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)
GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCCTTCGTAAATTACGGAATCA
CATAGCTTTTCATTTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC
TACAGGGTCTGACATTTTAACTTTCAGGTTAATGATGGTGTTCTTACTATATTTCTCGAG
TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTACTTC
AACTTTACCTTCCCTATACCTGTGTCTCTTATTAATTCAAGTTAATCCGAGGTAATAGA
TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCTT
GGAAAAGAATAACAATTAAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC
GTGTTCAACAACAATAAGAAATGGAGACCAGTTCCTTTGAGAATGCTCCTCCTGCAGCCA
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC
AATCTATCGAACTAGAGATGCAATTGACAAAGAAACCGGTGTGCAACGGAAACCTTCAAG
AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAATGGTGCTTTGGACGATGATGTTATCCCAATGCTATTGTTATTAATAAACATTCCGT
TTGCTATTAAAAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCCTTCTT
ATGCCTTCAATTACCACTTTGATAACGGTATTTTTCAGAGGACTAGCCTTTGCGAATTTCA
CCACTCCTGAAGAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA
GGAAATTGAAAGTGGAATATAAAAAATGCTTCCCCAAGCTGAAAGAGAAAGAATCGAGA
GGGAGAAGAGAGAGAAAAGAGGACAATTAGAAGAACAACACAGATCGTCATCTAATCTTT
CTTTGGATTCTTTATCTAAATGAGTGGAAGCGGAAACAATAATACTTCTAACAATCAAT
TATCTCGACTCTAATGAACGGCATTAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACCATTAAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTCTGAACCAAC
CTTCACTTTCTGCCCAACATACTTCTTCATCGTTGTACCAAACAAACGTTAATAATCAAG
CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGCCTCTCC
CACCCCAACAACCTGGACTTCAATGACCCTGACACTTTGGAAATTTATTCCCAATTATTGT
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCACAAGAGAATTATCAATGTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTTATTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC
AACAACAAGGTCAAATGACATCTGCTCATCCTTTGCAGCCAAACTCCACTGGCGGCTCCA
TGAATAGGTCACAATCTTATACAAGTTTGTACAGGCCCATGCAGCAGCTGCAGCGAATA
GTATTAGCAATCAGGCCGTTAACAATTCTTCCAACAGCAATACTATTAACAGTAATAACG
GTAACGGTAACAATGTCATCATTAATAACAATAGCGCCAGCTCAACACCAAAAATTTCTT
CACAGGACAATTTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA
GTTCTCAATACTAATTCGCGAGACCAACCGCAACCACTCAACCACAAACACAGCAAAATG
TTCAGTCAGCTGCGCAACAACAACATCTTTTTTAAAGACAACAAGCTACTTTAACACCAT
CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTATCAAATCAATTCCGTTAATCCCT
TACTGAGAAATTTCTCAAATTTCACTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACCTCAACAACGGGTACCAGTGGCATAACC
AAAATGCTTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACCT
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCATAATTTCTCATATC
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGCCGACTTGATCT
ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAAINDAQDNNINTETNDQETNQOSIETRDAIDKENGVTETGENSAKNA
EQNVSSSTNLNNAPTNGALDDDVIPNAIVIKNIPFAIKKEQLLDIEEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKKMLPQAERERIEREKREKR
GQLEEQRSSSNLSLDSLKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
NNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFDREKYYYELAYPMGISASHKRIINVLC SYLGLVEVYDPRFIIR
RKILDHANLQSHLQQQGMQTSAPLQPNSTGSGSMNRSQSYTSLQAHAAAAANSISNQAV
NNSSNSNTINSNNGNGNVIINNNSASSTPKISSQGFQSMQPTLTSPKMNIIHSSQYNNSA
DQPQQPQPQTQQNVQSAAQQQQSFLRQQATLTPSSRIPSGYSANHYQINSVNPLLRNSQI
SPPNSQIPINSQTLSSQAQPPAQSQQTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSOLLP
QHTNGSVHSNFSYQSYHDESMLSAPHLNSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGGTAATCGACGCCTTGCAATTGACTGACAAGGAGGGCGTAGTAACCTC
CAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTCCCTCTGTCTCCAATGATGAGG
CGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCTATTTAAGATTCACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA
ACTTTTATCTATCTTTTCACTTCTTATATATCTCATCTCGTACGAAGGGCCGCTCATTTGGA
TCATTTTCTTTTACATACCGTAAAGGAATGGCGTTAAAAATATATATATGAAAAATGCATG
TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC
TGCGTATACGCATTCTCGTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAAATTTCC
CTCATCCTTGCTCCAGATGCGAAAAAATTTGGTCTCCACTGTGAAATCAATCCTCAATTCA
GGCCTAAGAAGGGCTCACAGTTGCAACTGTGAGACAAAGATGTGGATGAAATCAAATCTA
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCTGTTTATCTTTTACAAACAGATTCCCA
TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACCTCCAACCTCCGGGTACTATTA
TCCCTAACCCAGATTCTTCTCCTTCCCTCAGGTTCTCCAACCTTCTTCCGCGGCTCAACGAG
ATTCTAAGGTTTCAAGTTCAAACCTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC
AGGCAGCAATACGAATAAAATTTAAAGCAAATAATGAAGCATCTTCTCACATGACGTTGC
GCGCATCTTCTTTAGCGCAAGATTGCAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC
CCCCGCTGCTAAATGACTCAGCATTCCTTAATAATTCAAAAGAATCTTTACCTCCTGCTT
TGCAAATGGCTTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCCCTTCTCTC
CAATTCAAAAAACATATTCCCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC
AACCACCATTTGCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA
CGCCGGTAGTAGCCACCACCACGACTATGCCATTATTGCCTTCGCCGCATGCAAAATGTAG
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA
TTTTCGTGACTAGGTATCTGCCGTATTTTCTTATTATGTATTCCAATAACGCCACCGAAT
TATAC'TCCCAATCTCAGTTGCTTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC
CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACACCTAGATCCACACATATTTGCAAGCTTTGTAAATATTGTGCATTT
GGCCTTTGCCTAACC AAAAGTCTTAGATGATTGTTCTTACCGTTTTGTAGGATTAGCAA
AGTCACTGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA
CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAAC'TAGGACTTGGCTGGGAATATTTT
TTGCCGAACTTTGTTGGGCGAGTATCCTTGGTTTGGCCACCAACTTCACAGACAGACTATT
TATTAGAAAAAGCCTTATCCTGTGGTGAGCAAGAATCAGAAGAAGATAACAATGACAGTA
TTGACAATAACAACAATGATAAAAGGAACAGAAAGACGAGCCGACGTTGAAAGATAAT
ACAAACTACCGGGCAGTTTTTAGAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAATTTGT
CTCATATCATTTGGTTCTTCCACTTCCAGTCCTGATGGTTTTATTGGAACCAAGTATCGTG

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACTTTAAATTTCC
AGAGTGACGATACTGTCAACATTTATTTTCTTTATGTTAAATTAAGTGTCTGTTGTTTGTG
CATTCCTACCCGAAACACCTCCTACCGATCAAATTTCCATATGTCACAGAGGCCTATCTAA
CAGCTACTAAAATTGTCACTCTATTGAATAATCTTTTAGAAACACACCAATTAATTGAAC
TGCCATTTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTTGCAGT
TGACTCCTTTACTTCTGACAAATATTTTGATTTCAGCAAGGCAATCCGTGGTCACTATCC
ATAGACTTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTGAGAATGATATTTTCGA
GAAGTGAAGTATGTTAGAAAACTGAAGTTTCGTACTGATCATGCATCCAGAAATTTTGTG
TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG
ATTTGGTTTGGTGTGTTTACGAGGCGAGAAGAAGGGAAATGGATCCCGAATATAACAAGC
AAGCCTTAGAGAAAGCCGCTAAGAAAAGAAAATTTTCTCAAATGGTATCTACAATGGCA
CTTCGTACTACGGGTGGCATAACGGACAGAAAACTATATCCATTGCCACTATATAACCATA
TCTCCAGAGATGACTTTGAACTGTAACAAAAACAACACCAAGTGAACCACTGTTACCA
CTTTAGTTCTTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG
GAGATTCTGACGGTTCTATAATGGAGATTAACGGGATACCTCTTTCCATGCTCGGGGAAA
CAGGCAGCGTAAAATTTCAAAGTTTATTCGCTAATACCTCGAATAGTAACGATTATAATA
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCTCTAATTTCAATTTATC
CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA
GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
ATCATTTTCTTCCGTCGTTCCAGGGTTAAGGAACCAACCCCGTTGGCAACTTATCTAATA
ATGTTACATTTGGAATAGACCACCTATTCCAAAGGAGCACAGTAATTTACAAAATGTCA
CCATGAATTATAATAATCAATTCAGCAACGCCAAGCGATTGGAAGATCACAAAGTAGTA
TGTCCCATTCACGTACACCTTTGTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA
CCCCGGTCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRSDSDQDFSSAHMKRQPEQQQLQHQFSPSKQRISHHDDSHQINHRPVTSC₁THC
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQQLLRQDVDEIKSKLDTLLA
NDSVVFVHLLQQIPMGNSLLNKLNLHPTPTPGTII PNPDSPPSSGSPTSSAAQRDSKVSQ
TYLSREPQLLOANQGSNTNKFANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLNDS
ALPNNSKESLPPALQMAFYKNNSAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPFFAAT
SHVATNNNADRTKTPVVATTTTmplLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL
PYFPIMYSNNATELYSQSQLLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWI₁RTPR
STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN
AEKWRTRTWLGIFFAELCWASILGLPPTSTQDYLLEKALSCGDEESEEDNNDSDNNND
KRKKKDEPHVESKYKLPGSFRRLSLANFQA₁KLSHIIGSSSTSPDGLLEPKYRAETLSIL
GKELDLLAKTLNFQSDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKI₁VT
LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLL₁PKYFDSARQSVVTI₁HRLYRNQ
LTAWATSVENDISRTASMLEKLNFLIMHPEVFVEEDGII SRMRSHLTGSLFYDLVWC₁VH
EARREMDPEYNKQALEKAAK₁KRFSSNGIYNGTSSTGGITDRKLYPLPLYNHI₁SRDDFE
TVTKTTPSGTTVTTLVPTKNALKQAEKLA₁TNNGSDSGSIMEINGIPLSMLGETGSVK₁FQ
SLFANTSNNDYNNR₁TL₁LDASNDISIPNSIYPVASVPASN₁NPQSTKVDYYSNGPS₁VI
PDL₁SMKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNV₁TMN₁YNNQ
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPT₁PVL

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCCAATTGGTGATGAAGAACAATCTATTAATGACACCAATTTCAAATTAAGTGTTC₁CA
AATTATGAAAACAAC₁TCATATAAAATACGTACAAATTTTCTCTACTCGAAGTGA₁TAGA
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAACTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGGTT
ATTTTCGGCGGCGGCAAAAATATTTGGTATAATTATGGAAATACAAAAAGGGGAACCAT₁T
AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAATCATA₁AA
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTGAAAAAA
GGAAGGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTGCG
AAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCGTAAATATCTAGTTCCTGTG
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAAGAGAATTATGCTACCCCTGAGA
AGGCCATCTTCATTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATA

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGLYVTYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCTGT
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA
AAGTGCTTTTTCAAGCATTGCTTGATTCTAGAAAGATCGATGGTTATCCCTCCCCCTT
ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTCGCACTTAGCGTGCTCGCA
ACACAAAATTAAGTAATATGCGAGTTTTAGATGTCCTTGCGGATCTATGCACGTTCTTGA
TGCGTATTTTATAACAACGGTTCTTTTTACCCCTTATTCTAAACATATAAATAGGACCT
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTCATTCTACTCTCTTATACTAAT
AAAACCACCGATAAAGATATATCAGATCTCTATTTAAACAGGTATCCAAAAAAGCAAACA
AACAACTAAACAAATTAACATGTCATTTAACAGTCCATTTTTTTGATTTCTTTGACAACA
TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG
CACCAAGACGTCAGTTAGCAAACACACCCGCAAAGGATTCTACTGGCAAGGAAGTTGCTA
GACCAAATAACTATGCTGGCGCTCTTTATGATCCAGAGATGAAACCTTAGATGATTGGT
TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCTAGAAAGTGTCGAGTTC
CAGTTAGATATTTTGGACCATGACAACAACACGAGTTGAAAGTCGTGGTTCCCTGGTGTC
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCATAATTTTGGTTCTG
GTGAAATTCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA
ACATTAAAGCAGACTACGCAAATGGTGTTTTGACATTAACAGTTCCAAAATTGAAGCCTC
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTTCTTCTCAAGAATCGTGGGGTA
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFFDNINNEVDAFNRLLEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
ALYDPRDETLDWFDNDLSLFP SGFGFPRSVAVPVDILDHDNNYELKVVPVGVKSKKDID
IEYHQKNQILVSGEIPSTLNEESKDKVKVKESSSGKFKRVTLPDYPGVDADNIKADYA
NGVLTTLTVPKLKPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTTCTTCTCAAGAATCGTGGGGTA
ACTAAAGTGACCTGGCTCTATAGTGTTGTCCCTCTCGCGAGGACCATTGTTGCTTGCCATA
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA
TATATGAGTTGATGAATAAATAGTTATAAAAACCTTGCTTTGGCTTCGATATATGACCGTT
ATTTTTGACTAAGTTTTAACGAAGGAATCTAACCTCGTTCTTGTAATTACCAAATCTTC
AACACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA
CTTCTACTTCTGGGAAAGGCATTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA
AAAAATAAAACGCGAAGAGCTAAAAAAGAAACCTACTATAAATAACCGATTAG
AATCGAGTTTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA
TCCTACAGGAGGTAAAAACAGCTCGGTATATCAAACGGTATTTGATTCCGGTACTACTC
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA
ATAAGTACACACAACTCAAACCAACCGCCACTGCAGTCACAACAGCCCCATATCTAAAG
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTTCGGCGGGACCTACTTTAAATCTTGCCA
AGAAGCCGAATAATCTGTCCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA
AGCCTACTACCAAAAAAGCACAAGACTTGAGTGTTGATGGCTACGCTACCTTAAAGCCA
GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGTCTAC
CAAGTGATTACAGATTCTCTCTCGAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT
TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA
ACATGGGAAATCCAGCCACCGACCACAAGCACAACAGAAACAGTGCCCTTCTACGAAGA
ATGACGGTGGCAAATACCAAATGCCTCTGTCTCAGCTGTTTTCACTAAACACTGTGAAAA
GATTCAAATCAGTAAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACCAGTC
AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCTA
TAGTAATGAACAAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA
AATTCCTTGCGCCCTCATCAGAGGGAAGGGGTGAAGTTCATGTATGATTGCTTAATGGGCT
TGGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

AAAATGACTCAGATATTAGTGGATGCCTTTTGGCTGATGATATGGGTTTAGGTAAAACAC
TAATGAGTATAACTTTTGATTGGACATTAATTAGGCAAACCTCTTTTGCATCAAAAGTTT
CATGTTTCGCAATCAGGCATACCATTAACTGGACTTTGTAAGAAGATTTTAGTCGTTTGTC
CCGTTACTTTAATAGGAAATTTGGAAGAGAAATTTGGAAGATGGTTAAATTTGTCAAGAA
TAGGTGTTTTGACATTAAGCTCAAGGAATTCCTCTGATATGGATAAAATGGCTGTCAGAA
ATTTTTTAAAGTGCAACGAACCTTATCAAGTCTTGATTATTGGCTACGAAAAACCTCTTGA
GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
GCCATCGACTAAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
GAAGGAAGCTTTTGCTTACGGGAACCTCTATACAAAATGATCTTAATGAGTTTTTCTACTA
TTATAGATTTTCATAAACCCAGGAATCCTTGGGAAGCTTCGCTTCTTTCAAAGAAGATTCA
TTATCCCTATAACTAGAGCCAGAGACACTGCAAACAGATACAACGAAGAATTGTTGGAAA
AGGGGGAAGAAAGGTCAAAAGAGATGATAGAAATTACGAAAAGATTTATTTTGAGACGAA
CAAATGCGATTTTAGAAAAGTACCTTCCTCCAAAGACGGATATAATTTTATTCTGTAAAC
CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG
GACAATTGACGTTTCAGTTCTTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAAC
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC
AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAATGACATTACTAG
AAGGTATTAGGAAGGGTACCAAGGAGAAGGTCGTCGTAAGTGTCTAACTACACTCAAACAT
TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT
CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT
TTGGATTCTTTGTTGAGTGCAAAATCGGGAGGTGTAGGATTGAATCTAGTCGGTTCGTTGCG
GACTTATTTTATTTGATAATGATTGGAATCCTTCAGTAGATTGCAAGCGATGTCACGAA
TTCATAGAGATGGTCAAAAAAGCCGTGCTTCATATATAGACTTGTCACAACTGGGTGTA
TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT
TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTTCAAAAAGAAAA
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATTGTCTCG
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG
ATTCTGTTACCCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAGCCCGCGGAGATAT
GTCTCAGAGAACAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQUIPKYENKPFKPPRRVGSNKYTQLK
PTATAVTTAPI SKAKVTNVLKRSISAGPTLNLAKKPNNLSSNENTRYFTIMYRKPTTKKH
KTWSGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSLSLFFETLFKAGSNEVQLDYELKE
NAEIRSAKEALSONMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVSRFKSVTK
QTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIMNKNAAAEVDVIVDPLLGLKFLRPHQ
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLGKTLMSITLI
WTLIRQTPFASKVSCSQSGIPLTGLCKKILVVCVPTLIGNWKREFGKWLNLNRIGVLTLS
SRNSPDMDKMAVRNFKLVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDEGHRKNG
ASKILNLTLSLDIRRKLTLTGTPIQNDLNEFFTIIIDFINPGILGSFASFRRFIIPIIRA
RDTANRYNEELLEKGEERSKEMIEITKRFILRRTNAILEKYLPPKTDIILFCKPYSQQIL
AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDPYKSHIKDTQSQDSYSRS
LNSGKLKVLMTLLEGIRKGTKEKVVVVSNTQTLDIIENLMNMAGMSHCRLDGSI PAKQR
DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK
KPCFIYRLVTTGCIIDEKILQROLMKNSLSQKFLGDSEMRNKESSNDDLNFKEDLKDLFSV
HTDTKSNTHDLICSDGLGEEIEYPETNQOQNTVELRKRSTTTWTSALDLQKKMNEAATN
DDAKKSQYIRQLVHYKHIDPARQDELFEVITDSFTELKDSITFAFVKPGEICLREQ

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTAAACAGCACGAAGCATATTATTGCGCATAATTTGTTCTTGTAGGATCTTTTC
TTGACATTTTTTTTCACTCTGCGAGAACTTCTCTTTTTTTTTCTCTCTAGGGACGAAAA
CAACAAGGGCACTTTTTTTTATCTTTTTTTTTTCTCTGTTGTTTTCAAACAAAAAGAT
TCCACCACATACATCAGTGTGAAAGACTGTAAAGCTTTCTGATAAATAAGCACTTTCCAT
ATTTTTCAACTGAAAAATAGTTTTCTTTTTCAGCTATTATTGACTTCATTAAAGAAATAT
CCCTTTTTTCCCCGTTGCAATTATTCTTATAAGGGAAGCTGGAAATAGGGGGCTGGAAAA
GATATTTGAACAGTCGCTCCAATAACCGTTCTCACCATCATTAACATTTTTGAAGGTGAA
TACTGTTTTCGGTCGATTTATGGCTAATTTGTCAAATACATTGAAAAAGATTAAAACAAG

CACAAGCGGTTGAGCATACTATGTCGCAGACAATTACATCTCTAGATCCGAATTGTGTTA
TTGTATTCAATAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT
TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA
GAATCCATCAGGATAATGCGAAACCGCTTTTTTTCATTTTTGCGAATCTGGACTTCATTG
AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTGCATAAACTGATTTCTA
TCAGCAAATCAAAAATACTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
TGACCAATAATCCCAAACATCCTTATATTTTGCATTCTTACAGAACTATATAAAAAGGT
TGATTTCCCTTCTCCTTTTTTGGATTATCAAAATTAGATTTTTATCTAATTTTACGTATGAAT
TCAATTCCACATACTCGCTGTTCCGCATCCTATGGACATTGTCATTTACAGCCTTTTGGC
TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTCTACCA
TTGAGTTTCTTCAAGATAAACAGAAAGCCCAAAAAAAGCTAGTTTCGGTTATCATGTTGA
AGAAATGTTGTTTTATTCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTTCCAGC
TATATTGTTTTTGGCTTGGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA
TCTTGTCTTTTTTGCCTACTATACTTATTGTCACGTTTACTCCGTTTTTAACTGTGATTT
ACAACAAATATTTCGTAGAACCAATGACAAAGTGGGAAATCATAGCAGTGTGTGAATG
CAAAGAAATCTAAAGAAGCTAAGAACCTTGTATTATTTTTTCTATCCAGTTACGTTCCCC
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTTGTTGACCGCAGAAATAAGAA
CTAAGGTTTTCAATGCCTTTTCAATATTGGCCCGTTTACCTACCCATGATTCAGATTTTA
TTATTGATACAAAGCGCTATGAAGATCAATTTTTCTACTTTATTGTTATCAACCAACTGA
TTCAATTTAGCATGGAAAACCTTGTTCGAAGCCTTGTAGCATGCTCAGCAGAAAATTA
ATGGACCAAATCCTAACTTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAACAGACCCCTGGGGAGCAA
CATTTGATTTGGACGCCAACTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTATTGT
TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT
ACGATAAGCCATCCTCTGTGTCTAATACCCAAAAACTGACGGTTGGTCTATGGAACCTCTG
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTTGACCTATATGTACC
AGAGCTGTAATATACCAGGTGTCGGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT
ACCTAGCAAATCCAATAAACCACTCGTGGATAAAATATTGTACTATATGCTGTTTTTATTG
AGCATGTTAGTTGTGCTATTTCTTCTTTCTCTAGTATTTTGAAATCTTCCCATGATG
ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAAACCCACCAAAACAAG
AAGTCTTTGAAAAAATTCCCTCCCCTGAATTTAATTGCAATAACGAAAAAGAACTAGTTC
AAAGAAAAGGGTCTGCGAATGAGAAGTTGCACCAAGAACTCGGTGAGAAACAGCCTGCCT
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAAATGATCCGTCTTCTT
TATCCTCAGCTTCTCGCCTTCATTATCTTCTTCTTCTTAGCAGCAAAACCGGTGTAG
TCAAAGCTGTTGATAACGATACAGCCGATCTGCTGGTAAAAAGCCATTGGCCACGAAAA
GTACTGAAAAAAGAAATTTCTTTGGTGAAGGTGCCACCGTTGGCTCATATGGTGTGCGG
GCGCCACTTTACCAGAAACAATTCCAACATCTAAAAATTACTACTTAAGGTTTGATGAGG
ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA
ACACCTTAGGCACGGAAAGTAAGCTTTTGCCAGATGGTGACGCCGTTGATGCACTAAGTA
GAAAAATTGATCAAATACCCAAAATTGCTGTTACTGGTGGCGAAAATAACGAAAATACCC
AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAAGATGCAAAATATTAAGCCTG
TTGTCAACGCAGCTGTTAACGATAACCAATCGAAGGTTTCAGTGGCTACTGAACAAACAA
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAACTA
AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACTACAGATGCTACTC
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA
ACAATTC TAAGACAACCGAATCCTCTTCTCTTCATCGGCGGCAAAGGAAAAACCAAAAC
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)

MSQTITSLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDTLSDDLHLKLSISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF
WSDRLSKYSSFSTIEFLQDKQKAQKKASSVIMLKKCCFIPVALLFGAILLSFQLYCFALE
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSSVNNAKSKEA
KNFVIIFLSSYVPLLITLFLYLPMPHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY
EDQVFFIVINQLIQFSMENFVPSLVISIAQKQINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVFSYQTDPFWDLDANFKLLQLQFGYLVMFSTIWLAPFICLIVNLIVYQVDDLKRA
VLYSKPEYFPFPIYDKPSSVSNTQKLTVGLWNSVLVMSILGCVITATLTMYQSCNIPG
VGAHTSIHTNKAWYLANPINHSWINIVLYAVFIEHVSVAIFFLFSSILKSSHDDVANGIV

PKHVNVNQNPVKQEVFEKIPSPFNSNNEKELVQRKGSANEKHLHQELGEKQPASSANGYE
AHAATHANNDPSSLSSASSPSLSSSSSSSSSKTGVVKAVDNDTAGSAGKKPLATESTTEKRNS
LVKVPTVGSYGVAGATLPETIPTSKNYLRFDEDEGKSIRDAKSSAESSNATNNNTLGTES
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTTDTATQPHHHHH
HHRHRDAGVKNVTNNSKTTESSSSSSAAKEKPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)

ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC
GTCTATAAACTTCAAACGAAGGTAAAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG
AAATATATATATAAATTAGCACGTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG
TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG
GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCCGAAGA
GATCGCACATGCCAAATTATCAAATTGGTCACCTTACTTGGCAAGGCATATACCCATTTG
GGATAAGGGTAAACATCTTTGAATTGTGCGAAATGAAACGTATATAAGCGCTGATGTTTTG
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAATAGAGC
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT
TGGCCAATGCAGGTACCATTCCCTTAGGCAAACCTAGCCGATGTCGACAAGATTGGTACCC
AAAAAGATATCTTCCCATTTTTTGGGTGGTGCCGACCATACTACTCTTTCCCTGGCGACT
ATGGTATTTCTCGTGATTTGCCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA
GACATGGTGAAAGATACCCCTACTGTCAGTCTGGCTAAGACTATCAAGAGTACATGGTATA
AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTGTTCATTCTTTGAACGATGATTACG
AGTTTTTTCATCCGTGATGACGATGATTTGGAATGGAACCAC'TTTTGCCAACCTCGGACG
ATGTTTTGAACCCATACACTGGTGAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG
CTCAATACGGTTACATGGTCGAAAACCAACCAGTTTCGCCGTTTTTACCTCTAATTCTA
AGAGATGTCATGACACTGCTCAATATTTTCAATTGATGGTTTAGGTGACCAATTCAACATCA
CCTTGACAGACTGTCAGTGAAGCTGAATCCGCTGGTGCCAACACTTTGAGTGCTTGTAAC
CATGTCCTGCTTGGGACTACGATGCCAATGATGACATTGTAAATGAATACGACACAACCT
ACTTGGATGAGATTGCCAAGAGATTGCAAGGAAAGGAAACAAGGGTTTGAACCTGACCTCAA
CTGACGCTAGTACTTTTATCTCGTGGTGTGCATTTGAAGTGAACGCTAAAGGTTACAGTG
ATGTCTGTGATATTTTACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC
ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCGGTTCCAACCTTGT
TCAATGCCCTCAGTCAAATTATTAAGCAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA
GTTTTACCCACGATACCGATATCCTAAACTTTTTTGACCACCGCTGGTATAATTGACGACA
AAAACAACCTTAAGTCCGAATACGTTCCATTATGGGCAACACTTTCCACAGATCCTGGT
ACGTTCCCTCAAGGTGCTCGTGTCTACACCGGAAATTCGAATGTTCTAACGACACCTACG
TCAGATACGTCATTAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT
TCCTAAAGGTCTGTAACGTCAGCAGCGTCAGTAACCTCTACTGAATTGACCTTCTACTGGG
ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)

MFKSVVYSILAASLANAGTIPLGKLADVDKIGTQKDIFPFLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPYTGEMNAKRHARDFLAQGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSVCDIFTKDELVHYSYQDLHTYYHEG
PGYDIKSVGSNLFNASVKLLKQSEIQDQKVWLSFTHDITDILNFLTLAGIIDDKNLTAE
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVPIETCSTGPGFSCEIND
FYDYAEKRVAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
859-1563 (SEQ ID NO 21)

TAACTTCTCAACATAATTATGTAAAAAATTATCTCATTAAGCCAGATAGCAAATATATCA
CATATTGCATTGATTAATTTGAGAAAAATATACATGTATCTTTTCAGTTAATTTTATTAA
AAATAAATTATTTTCTTACTTTTTTTTCTACAGTTTGCACCATTAACTCTTTTCTTGCA
TCCATACATCTTTGAACTCCATACATCTTATTTTTTTTGGCTGTTTTTTTTCAGTGCTCGG
GCATACAGCCGCTTATCTTCATGCCGCCCATCATCTAGGAAACTCTTTCGGTATGGG
CCAAGGGCAGGCGAAAAATCCTATGTGCGTGGAGCTGATACAATCTCGGCTGGCTTGGTTT
GTAGGGCACGGTCAATGAATGCCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCTAA
TGAATCAGCAGCGCTAACCGGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT
AGTGCACCTATAATAAAAATTCTCAAGAACAACGTGTTTAAACGAGATAATTCCCTCTAA
TATACACGTACCGACACTTAGGAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAAAAGAAAAAACCTGTAACGGAAGAA
AGGACAGCAGGGATTTCGTTGGAATTTGTTCGATATTGGCTTCGGACAACCTTTACTAACAAA
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAGACCTTC
GAAATTGATGATGAACACCGTATTTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTC
GATGGTGAAGCCGTTGGTGTGAATTCAAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC
GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTG
TTGACCAAGAACGTTTCTTGTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAAGTCC
GTCAGAGGTGCCATTGTTGGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAG
GGTGAACAAGAATTGGAAGGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAG
AGAGCTAACAAACATCAGAAAAGTTCTTCGGTTTGTCTCCAAAGGAAGATGACGTTTCGTGATTTC
GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGGTTACTCCTCAAAGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTCAGA
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG
TCTGAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVGDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD LAVLALVIVKKGEQE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKEKTYTKAPKIQRLVT
PQRLQRKRHRQALKVRNAQAQREAAEYAQLLAKRLSERKAEKAEIRKRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTTTGTGC
AGTGTATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT
TAAAACGCTTCCACGGGACATGGGTTCATAATTATGGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC
TATCAGTATATACTCATTGTGTTTTTCAAAAATCTCTGGGTGTTTGTAGATGCCACTATA
TTTCTATTTCGTATTTATTTTATGTATACTTATTTTGCTTATTTTCTTATACTCAGGAA
ACGTCATTGGCTTGATATACTCGACGCTTTATTTCTGCAAATTCAGGTCTCAAATTCGAA
CGGCTGGAGCCCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCACATCAAAAAC
ATCATGGCCAATGTCAAATCACTGTACTTCTCCAAACACTGTACGACAAAACAAAACAA
ACAAACTCTTGTAGTAAAAAAGAAAGGGAAACTAGTAATATGGAGACACATCGTAAAAA
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCACGGACATG
GCACTAACCACTATGAATACACCAACAACAGTATAGCTAAATTTGGACGCGCAGAGAGTTA
GTAGAAGAAGAAGGAAGAAAAGGGAAAGCGGAGAGAAGAGATTATGACACATACAACTAC
TCATTACTCTTTGTTCTTTATTTATTCGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)

MELAKERNPHQKHGQCQNHCTSPNTVRQNKTNKLLLVKKKGKLVWRHIVKKMLHIRL
VVLWSHYPEQHGHTNHYEYTNNSIAKLDAQRVSRRRRKKREAERRDYDTYKLLITLCSL
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)

ACATGACCTAATTTATAGCTTAGGGTCTTTTTTGTCAATTCTATGCGTATGACAAAGA
GCACCACGATGGTGTATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG
TAGGCGGTTTATTATCTTTGTCCCTTTATACTGTTGTGTTTCTTGCTTATTGCTTCAGTA
GGCAGCGTATAGTATAACCAGAAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG
AACGGTAAAAATCCACCAGAGATTTGCTCACTAATAATCCTGTACCATGTCCATCAACCT
ACATTCGCGACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT
GGATATAATAACAGGATCCGGTTCAAAATCACCAGTTAAGGTTTAAGTCATTGGACAAAGA
CAAGTCTGAAGTTGTACTGTGTTTCGCACGACAAGACTTGGGTGCTGCAAGCAGCGCAAAC
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTCTTGAACAACCTATTACTTTTCGACG
AAACGCTCTTGTGTTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTCGCCAAGACTG

AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT
ACAACGGAGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCTTGGAGAAGTACTTGTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTTGTGTATTCTTTTCAAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTTCAATC
CATACACAAGAGAAATCATTTGAAACAGTGTGAATAAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA
AGTCCCTTTTCCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA
AGCCTCTAATTGAAGAACTAAATTCAAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCCCGCTAAAAGACTGGGCAAAAAGACCGTGGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)

MREFVPEQPITFDETLFLGLSKPYMDVVGFAKTESEFETRETHGELNLSVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENSSPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAEGLDLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFVQEQEAENNTWR
LRIPFIAQWYGIQALRKYVSGISMPIDEFLIKWKSFPFPFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLRPMDPKERFKVLFRLQSQWDLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)

GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAAAAT
GACCCTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC
ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAGGTACATCCGTGCTATGGTCAGAGAG
CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCGGGGACGAACCAGATTCCAAGAGAAGA
AATAACGACCCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA
CATGAAGTACTTCTTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA
TAGACGTTCTTACAAGGTAAAATTTACCGCGTTTTTTAAATAGAATGAAAAAACGTTGT
AGAGTGAAAGAAAAGCAACAAATATACAGTTTACAAGGCAGCTTCGTATAGTAATACAGC
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA
CGGATGCTTATATCCCCACGTATCTGCCCCGATGATAAGGTCTCCAATCTGGCAGATTTGA
AAAAATTGATAGAAATGGATTCCAGACTAGATTTGTATCTGACAAGAAGGAGGCTGGATA
CGTCCATCAATTTACCTACAACACCAAGGACCAAGGACCATCCCCCAATAAAGAGATGC
TGAGGATTTTACGTCTACAACACTACGGAAGCAGCCCTCGCAGCGATTCTGGCACCCAG
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG
CAAACGGAAAGCACCCATTTAGTGAGTTTTTGGAAAGGTGTCGCGGTGACTTTTAAAGAC
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACGCGATTTCGTATTGAGCCTTCCTTTGA
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG
AGGATGAGGACAGTGCAGAGGCAGAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA
ACTACGATGAAAACAACGTTGTGGAGTTTGTATGGTATCGACATCAAGAGGCAAGGCAAGG
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAGTACAGT
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT
ATTGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACGGAACAAACAGAGGCTC
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG
GTGACGATGATGGCGTCGAGGGAAAGTACTCCAAAGGATAAGCCCGAATTGGGTGAAGTGA
AGCTAGATTCACCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCTTGATGA
ATGTTGTGCAAAACCGTGAACAACTGGTATCACCCTACCGCCCATCATCTAGATTATA
CATTTGATCTTTCCAAAGATACCACTTATGGTGTCTACCACCTTGGATGTAGATGTGTCGC
ACATTTCTCCACCAGCTCAACCCAGCCAAATTTACAAAAAGAGGAAGAAACAGATGCTG
AAGACACAGCAAACTACGTGAAATCACAAAGCTTGCCTTGACAGTTGAACCTTAGTGCTC
AAAAATACCAGTTTTTCCACGAACTGTCTTTGCATCCAAGAGAAACGCTGACTCACTACT
TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGAACGAGTGACATATACAGTAACAACAATGACAGGTCACTAATGGGCAATA
TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNVPVPVPTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRLDTSINLPT

NTKTKDHPPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF
SEFLEGVAVDFKRLKPLGMGKKRKRDSLSLPLNLQQPEYNDQDSTMGDNDNGEDED
AESREEIVDALEWNYDENNVVEFDGIDIKRQKDNLRCSITIQLRGVDGGKVQYSPNLAT
LIGMQTGSVNDAVYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDDGVE
GSTPKDKPELGEVKLDSLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYTTIDLSKD
TTYGATTTLDVDVSHILHQPPQPNLQKEETDAEDTAKLREITKLALQLNSSAQYQFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTAAACGCGTTATCTTTGTTCCGAAAAAAGGAAAAATATATTTTTTC
GCGTCGCGTTCTCGCGTCTGTTTTGTTTTTCGCGTTCCAATGACCAAAATGGGAAAGTG
GTCGTCTTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC
AGCCGCAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTGCGTGTCTTCTCCT
CTAACTGTGCACGAGGCACCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTTT
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGTTTTTGCGCCATTTGGCAATTAGCA
ATTTATCAGCATACTTTTTCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTC
TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC
AGAGCTGCTCATTTGGACTTTGCTGCGAGCTTAGACGACTTGTCTTTTGGGCATCTCTGA
GTTGGATTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTGCAGCT
TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTTGTGAGGTGAGCTTTGCTAGTCTTG
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTC
AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA
TCATCGTCAAAGTTCCTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWWSCIISQCSLDFAASLDDLSFWASLSWISKSVRVGLIFSNPSGAGLDLLVFM
RGMSFCEVSFASLDGCRGVYIDDESLRKFFFFFQYFTFR CERQMYAFKSQRSIIIVKVPT
TTRVIDLVLVNVNLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCCGCTTCAGCCGCTTTTGTGTGCTGTGTATTTCAGTATATCCATCATCA
TTTTACCTACAAGGAACCTACCTTTTATAGCCACCTAAGTAAAACAACATTAGCTTAGC
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTCTGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTTCAATTTCGAGACAT
AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAAATGAAGAAAATGTGATTAGA
CATCCTGGGGAAATTAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTCTAACAAATTT
CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA
GCAATTTGTCAGCAAGACAATATGACTACGACGGTACCCTAAGATATTTCGCGTTTCACGAGT
TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCCTGGATATGA
CGAGAGAGGCCCTCTTGCAAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG
GTAGTGGCAGTGGTAGCAGTAAGCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG
GTGGGTCAATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA
ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAACCTC
CGAAGGTGTACCACATTGACGAGTCAATTGATTGACGACCCGCAAGAATGCGTTGATAACT
ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCCGTCAAACCTCCGATGTTCCG
ACTTGTTCCTGCTTGGTTGTGCCCCGATGGTCATATCGCATCACTCTTCCCTAACTTCC
AGGACAATCTACGTGAGAACTTGCATGGGTGGTGGCCGTGGAGAACGCTCCTAGTGGGC
CCTCGACCAGAATTTGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTTCG
TTGTGCAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAAGGCCTGAAAAGG
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTGTGATCATGTTTGTGACG
ACGATGCTCTTACGGACGTCTCGTCAACAAAAAAGTATAAATTCACCAAGGTTTGT
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTPVKIFAFHEFSDVAEAVADHVVHAQD GALAPKNERKHSVPNISMNALDMTREASCK
STASAAEGKSGSSGSGSSGSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVRWGDWDIYF
ADERLVPFSSNESNYGCARKILDLIDTAKYGT PKVYHIDESLIDDPQECVDNYEKVLIR
GFAGRDSVKLPMFDLFLGCPDGHIASLFPNFQDNLREKLAWVVPVENAPSGPSTRISL
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALTDV
LVTKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTTAACTA
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGACAGA
CTCAGCTACCGATTAGTGTTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC
TAGTCATCCCTCCACACAAGATTCGCTCTTAAGTAGTGGCGCAGGCTGTTGCGCTTTTAAG
CATAGTGCTTAATGTCTGAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAATTGAAT
GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGCGCCTGAGGCG
GAGCGTTGCGGAAATCGGGAACATTATACTGGGAAAGATCACTATCTATTCTCTAAAT
GAACTTTTAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT
AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAATTTTAAGCA
TTACAACGCTATTATTGTTGTTAGTGTTTTTCGTAGCGCAAAATGCGAACCTTCTTGACGG
TAGAGATAAAAAGAGGAACTTCTAAAGCATTTAGTACTAATATGGACAATATGGCTGGAG
GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG
TAGACGAAGAAATTAATGAAATAAAACAGAAAGGTGGGACTCCAACAGCCCATAGCATCGG
TTGATGATAGTTTGTCTCGGCCATTAAAAACGATAAAGGGTCGCGAATAACCAAAGCTTTTA
ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA
GCACCTGTTTCATATAGCAAGGGCATGAAGGAAGTCTTGAAAATGAGTATCAGTTTATCC
CAAACCTACTATATTATAGAAGTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA
TCAAGTTGGTGACCGGTAGAGGAAGTGTTCAAACCTTTTGGTTAATGGAGTATCAAGAG
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACCTTTTAGAATCATTACAAG
TCTGGAGTGATGGTAAATTCTCGGTTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNARILSITLLLLLFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA
AMPTSTTNKGSSEVDEEINEIKQKVGLQQPIASVDDSLSAIKNDKGSRITKAFNVQKEYS
LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYIIELDKHHGHEELQEYIKLVTGR
GTVPNLLVNGVSRGGNEEIKKLHTQGKLLESLQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAATCCAGCTTCTTTTCAAGCAATATTGTCAAAACGATGATGAGAATAGCATTGAAG
AGGATAAGAATTTACGCTATTTCAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA
CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
ATAGTAGCGGTATAGATTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTGTGTA
TCGCGATGTTTGAAAATGGAAAGTAAGGAACGTAAATACAAATTGACAAGTAGCCGACATG
AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTCATT
GAAGCAATGTGATTCTCTCGATAAGTAAGCTTTTTTCTGTCTGGCGGCGAACCATAGAG
AACAAAAGACCGAGTTAAGAAAAAGTTTCATAAAAAACCTTTGAAAATGGATGAGTGCTCG
TATAATGGAATAGGAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC
CAGTAATAATGGCTCGACAACTCAAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGACG
GTAATGCAACCTCAAATGAGTTTGATGAACATTTGCAAAATGAGGTTGAAAGAGAGAGGG
AAATTCAAAAAGAAAAAAATAAAGCGAAGTCAATCAAAAAAATCGCCAGATTTGATTA
ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAAGAGAAACATAGACAACCTAG
ATCCAGAGTATGAAATTGTCATCGATGGCCCTCTAAGGAAAATCAAGCCCTACCATTTTA
CGTACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAAATTGGTTGATGTCTTTATAT
CTGAATTTTCGAGATCGTGAATCTGAATATTATAAAAGAACAAATCGAAAACGGGGACGTT
ATATAAACGATGAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC
ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTGAAG
ATGATAACATAATGGTTATTGATAAAACCGAGCGGTATACCTGTTCAACCAACTGGCCGAT
ATCGGTTCAATACAATTACGAAAATGCTTCAAAATAATCTCGGATTTGTTGTGAACCCAT
GTAATAGGTTAGATAGGCTTACAAGTGGATTAATGTTTTTGGCAAAAACCTCCGAAGGGAG
CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAAGTCACTAAGGAATACGTGGCCAAGG
TAGTTGGAGAATTTCCAGAAACGGAAGTAATTGTTGAAAAACCTCTAAAACCTGATCGAGC
CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA

CTGTTTTTAAACAGAATCAGCTACGACGGTAAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT
GGTTCCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCTATC
TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNNRLRLNFTVPVIMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKKK
IKRTQSKKSPDLINKSTFQSRITGSKKEKRLDPEYEIVIDGPLRKIKPYHFTYRTFCK
ERWRDKKLVDVFISEFRDRESEYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPIKVIFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVVNPNCRDLRL
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGEFPETEVIVEKPLKLI EPR LALNA
VCQMDEKGAKHAKTVFNRI SYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EVWGNLNLGKGQADFDIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKC SICESDLYTD
PGPNLDLWLHAYLYESTETEEGTEKKKWCKYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
1342-1364 (SEQ ID NO 37)

TATTCGACTAGAAAAAATTAAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA
GGATGTAACAGGAAATGTATGGGTACATATTAATAGCTTGTTTACTCCATAAAAGAGT
CTGATATTTCAGAAAAACACCCATACATGTTGAAAAATAATGCATTTGTGAAAAAAGTGG
TTGAAAAATGTATGCGATCTAGGAAAACTGAATTTTCCTTAGGTTGTGCTCCTCCTCT
AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATCTCTCTGTTCCCTCTAGCTGAGG
GAAACAGAACTGGTAGCAGTTTCGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT
TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAATGTATA
GGTTACGCAGTAGACTATTTAATATATACCTTTTATTTAGCAGTGTTCGAAAAATACA
GCAAGAGAATAAGCAACAAGATGTCCTGCCGTCCCAAGTGTCCAAGTATGTTAAATAATTT
AAACGATGTACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA
AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTA
GAACAACGGATCACCATTTTCACACGTTAAAGACCGAGTAGAAATAACCAATAAATTTGTGT
GGGAAAATATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTTTCGGTCTT
ATTTATTCATTTCGCTCCCTTTGCAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC
CAGGGTACCTCACTTGTTTCACCCCTTTTACACAGTTCATAATATTTTGTAGGATTTTGAA
TTTCTGTTTTACTAACATGTGACACGAAATGTTTTCATTTTGGTTTTATAACAGACTT
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGTCAAGGCCGTAAGGGTTTGATTA
AGGTCACCGTTCTCCAATCACTTTGGTTGAACAGAAATCCTAAGATTCAAGGTCCTACG
AACCATTATTGTTGGTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA
CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG
TCGCTTACCACCAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA
CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAGAAATTCG
GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRTL LIAD
SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCGGTTAATTCTCCGCGCTTTTCGTTAGACTATTTTGAAGGACCCAAATAGGAG
ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGCGCAAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGTTCTACAGAACTTGAAGTACAAAAGGAGGTACATAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGCGAATCGTTACAGAATATTCCTTGAGAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGTAATGTGA
TGTGTGTTTCGACTGGAAAGCGGAGAACATTATGAAGTAAAAGGACAATCAGCACGCCTTC

CAGACTTTTAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAACAACAA
AAATGTCTGCTCCTGCTACGCTTGATGCTGCCTGTATTTTTTGTCAAGATTATTAAAAGTA
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATTCAT
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
AAGGTCATGCTTTAATCATTCCTAAGTACCATTGGTGCAGAGTTGCATGACATCCCGGACG
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
CTTATAATGTGTTGCAGAATAATGGTAAAATTGCGCATCAAGAAGTCGACCACGTCCACT
TCCATTTGATTCCTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG
AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATTGCTTGCCAAACTAGAAGGCT
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTHKMSAPATLDAACIFCKIIKSEIPSFKLIETKYSYAFLDIQPTAEGHA
LIIPKYHGAKLHDIPDEFITDAMPIAKRLAKAMKLDTYNVLQNNKGIAHQEVDHVHFHLI
PKRDEKSLIVGWPAQETDFDKLGKHLKELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTTGTGTTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAG
ACCTCTTCTCCTCTTTTCGACACTTCGTTTATTTCCACTTTCCCTTATTTAGTATTCATCG
TTCAGAATGCTTTCTTTATTTTCACGACGGTTACCACACCCGTACACCTTATCTCATTTTC
ACCAGTACCTTTCTTATTTAGATTTCATCTTATTTTATTTTAGGATTTTAGGTCATTTGTA
CGACGCGTGTGCGACCATGGAAAAGGTGTGCGAGCTGCGATGCTATCCATTTACCCGTCA
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTTATATATATGGAGAGTTA
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATTGTTTCACTTCTC
TCTTTGAAATTTTCGCTTGTTTTCTGTTTTTCATCTTATATTTTACTTCAATCCTAAGATAG
TCATATCGACTTAATTCCAAATGAGAGCTAAGTGGAGAAAAGAAGAGAAGTAGAAGACTTA
AGAGAAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRKRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2:
909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTCTTAGATTGTTTTATTTTATGATTGTTGAAGATAT
AAACCACGTATAGTTGTATAAGATAGGATAATGATGGTGCACCTGAAAATAAACTTACTA
GCTCTTTAATATTGCAACGGCTTGTAAACGGGCGCCATGATGACATTCAGAATTATACCAC
TACTATATGAAAAAATGAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATTCTATAATA
TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTTCAGCACCCAAACATTTGAATTTTTTTTCATGTCGATTGTGAAA
TTTTACTGAAGATGAGGGTAAATAGAGGCCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAAATCTACTCACATCTCTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA
AGAACCAAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA
TAATGTGCTATGGAAGAAAAAAGTCTCCTTTAATGTCTGCAGGATAAAATAATCAAGTGGT
CTGAAGAAAATTTACAGCTACAGTATTACTGCAAACCTTGCAGGCAAATATCAGAGAGAT
CTCACCAGCTACAACCTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAATTTGTT
TGGAAGTTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCACATGTGAACATTT
TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGTATACGAGAATCTAAAAATTTGAA
ACTGGCTCATAAAAACAGGAACCTTTACTAACAGTTATGATTTTTTGTTCCTTTCTTT
ATCAATAGGCCGGCGTTAAAGCTTACGAACAAAGAACCAAAATCCAAGGAACATTTAGCTT
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTCCAGAC
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA
ACGAACAACAAAGAGAAGCTGTTAGACAATTATACAAGGGTAAGAAGTACCAACCAAGG
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC
AAGTTACCGAAAAGCAAAGAAAGCAAAATCGCTTTCCCAAAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA
TGTGGTTAGAACCAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGAAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTTCTTT
AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC
GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTTCAACACATACAAGTTTAATAAGTT
GGTTTTGATGCAAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG
TGATTTTTGATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTC
CAGATACCCCCAAGGATCAATGTCGCATTGCGAATATAGCATTTCAAATTGTAATGCTG
AAACATTAGTATGCCATTATGGGACCAATTTTACCGAGCATTGAAGTAAACGGGACGA
CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA
ACGACGACTTTGTTCTTGTTCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTACAACATCCGAAAGTATTTG
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATATTGGAAGTTTCAATCCCACTGAAGAGGCAG
GCTCTGTTCCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAACTGC
ACAAAAAGTGTACTTCCCCGTAAGATATGGAATCTGTCTTAACAAAACCATGACTCAC
ACACCGATATTAGAGCGTTTTTGTCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC
CGCCCGACACAACCTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTAGACCAG
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATAACTGGA
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTTGTCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC
TGGCAAACACTAAGCAACCAAGGGTGGTGAACATGTCCTTGAGCTTCAACCTTCTTCCA
CCGGAGTACTCGATAAGGCTCAAGAAATTTTATCGCCTTTCCCTCAAAGTAAAAACAAAC
CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACCTTCAAAGACGTACTG
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAATACATACTGCGAACTCAA
ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACCTCGGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGCCCTGAGTTCAACATGATTG
CTAACACACGCCAGCAGCTTTAACATACATAGAGCTCATTTTCTTGCAATTACGCCAT
TGTCGCGACAAATTCATTGAACATGGCACCATCGAACAGTGGGTGCGCGATAATTATAG
CGGATCATTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAAATATTA
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAAATAACA
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTTCCAATATCGGTATGGGAGGAT
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCACGTGCACGTATCATA
ACTTTGTCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGCGCATG
CAAGTGAAACCAATCATTACATAGATTACATCAACATTGGGACCAGCGTACGCTATCCCA
GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTGCACCCGATGGGA
ACGATAACAAAGGTCGTGATATTAGTTTGATGGAATTTATGTCACCACCGTTATCGATGG
CAACAAAGTCAATGAAGGAGGAGATGGGAATGGTAGCTCGTTTAACGAGTTCAAAGTG
ACAAAGCTAACGTTAATTTTTCCAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTTA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVLELQVAHLPDTPKDQCRANIAFQIVNAETLVCHYGTSNLSPIEVNGTTKSLESA
MVQLDKDIHDVIGNDDFVLVSLYSTWHIRVTLPRQARDDGFILTSYLQHPKVFDLWKEFD
RWCNVNHEILGQKKAISNNCNTKSISINAANKTKDLDEIVRILEVSIPTTEEAGSVPEIY
SLLKRTTDILIQHLKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNNLPDTTQS
ELESWFTQYGVRPVGFWTVKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVFQTHEEAT
EVLALNGRSILSNLANTKQPRVVEHVLELPSSSTGVLDKAQEILSPFPQSKNKP RP GDWN
CPSCGFSNFQRRTACFRCSFPAPSNSQIHTANSNNNNVNSSRNNLNNRVNSGSSNISNTA
ANHPYGAPEFNMIANNTPAALTYNRAHFPAITPLSRQNSLNNMAPSNSGSPIIIDHFSGN
NNIAPNYRYNNNNINNNNNINNMNTNNRYNINNNINGNGNGNGNNSNNNNNNHNNNNHH
NGSINSNSNTNNNNNNNNNGNNSNNCNSNIGMGCGSNMPFRAGDWKCTCTYHNFKNV
CLRCGGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRTDGNDNKG

ISLMEFMSPPLSMATKSMKEGDNGSSSFNEFKSDKANVNF SNVGDNSAFNGFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCCTTCCGTTGATCTTAGATTTCTTAGAGGTTCATGAAC TAGAAAGCGAC
TTGAACAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAAATTTAATGTAGA
TTGTCCACTATCTCATGTAAATATACATAACAGGTATTCTTGAGCGTTCGAAAATTAGAC
TGTACTTTTCTGATGCGCTCCCGTACACCTTTGACATATACAAACATCCGCACATTTTAT
AGCTTTCTTTCTAGAAATTTTTTCCACGCGCTCTCGATCAATGAACCTCTTAAAAGTAACTG
ACCCCTAACTTTTTTCCCAGGCAAGGCTGGCCTCATTACCCTACCCGAAAGTTTCACTTTA
CCCCATGGCAGATGGACGATATTTTAACAAGACGAACTGACCTCGTCTTCTATAAACT
GGACTTCTAAGCAACTCTCATTATCTTATATCCGTTCCATTTTGTACTAAAAGAACCAG
ACCACATCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRAKWRKKRTRRLKRKRRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTCGCTCTCAGGTCCACCGTGTTCTCAAAAGATACTTTTAAAACCTAAAAC
ACACGAAATCATATTATGATAATTGAGATGATGTGGTACTGTGTCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAACCTTT
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTTAC
ATTTAATTTTTTATCACATAATAGGTAGCTTAAATTGTAAAGTCGCAAAAAAAAAATGGCA
GCGCAGCCTCTCCGGGTGAACCCACGACAACCTTACCTGGCACTCCATGCCTAACGGGC
GGGTTTGGGCAGGATTCCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT
GTAATATAATGTTAAGCATACGCTGTCGATTAGCACTATTATTGACCGTAGAATAGGTAC
AGTGAGACAGTATATTTCGAAATGGTATGTTTGAGATGAACAAAATAATAAAGACTGACAA
CTGCAGAACAGAGAGGATCATAGCAACCTAGTGCAGAAAGAGCCCTCGAAGCGTTAAACT
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATTATTTCGCAAGCAAAGAATCAAGGAAAAGAAAGTGAAAATAGC
ATACATCTTTAAATTCAGAGGTTTGTCTGAATTTTAATAGGGAAGTTTACGTTATGATTG
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCTCCTAATTTTTTTATTGTAAA
AAAGCCTTCCAACGAAATAAATTAGTTATTGGTTTTTTTTCTCTGTTACGAGGGATATAT
GATGCCTGTGCTTGTAGTTCAATTATAAGTGCTAATAAAATACTAACGTTAATAAAAATT
TGGAATATTATTTTCAATTTTTTATCCTATTAAATAGGCCGGTGTAAAGCTTACGAACTAAG
AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAAGAGAAGCTGTTAGACAATTATA
CAAGGGTAAGAAGTACCAACCAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGC
TTTCCCACAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKQYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTCTTTTAAAGGGATATATAACAGATTCTAAAACCTGACAGAAATATTTTCGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTTCCGCAAGTTCTACTCTGATACATTTTTGAAGT
AGGAGAGTCATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT
TAATTAATAAATAATAAAGGTAGTGATTAGACGACACATGTCCATAGGTAACCTGTCATAA
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTTGGGTGCGGCGATATGTAGCTTGTT
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAAATTTCTTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA
AATATTTTAAAACTGTTTTAACCCATCTAGCATCCGCGCTAAAAAAGGAAGATACAGGAT
ACAGCGGAAACAACCTTTTAAATGATGGAAACTCTACAGACAATATAGTTTCCCTTTTTC
ACAATTTTGGTAGCTCGACACAATATAGTGGTACCTTGTCGAGAACTCCCAACCAAATAA
TAGAGCTAGAGAAGCCAGTACTCTATCCCCATTGTCAAGAGGAAAAAAATGGACGGAAA
AGTTAGCCAGGTTCCAAAGAAGTAGTGCTAAAAAGAAAGATTCTCACCTTCTCCTATTT

CCTCCTCTACATTTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACCTCTTCTGGCA
ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC
ACCTCACAAGAACATCGTCTTTGCCAAGACCTAATCCAATCTCTTTCACGCAAGTAATA
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAATATACCAC
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAATAAATCCTTTTTGA
ATGCTTCTGTACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAGAAAATTA
TAGAGCTTGCATGTGGCCACTTAAGTCAACCAAGAATGTCTTATTATCTCTTTTGGCACCA
CTTCAAAGGCAGACGTTTCGTGCGCTATTTCTTTTTGTACCAAATGTAAAAAGATACTA
ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAACTAAAGGATATTCTAATTTCTGATT
TTTTGATTACATAAGATTCCCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCTCTC
CTTATTACCACTCTTGCCTCCTTTTGGGTATCCTATACACCTGTTGAAAGACAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA
GAAACCAAATTCACAAAAAAATCAAACCTATACATTTTACATTCACCCCTGGGGCACA
GAAGAATTCGTCGAGCAAACCTATCTTAGCAGACACCTCTGTAGCGTTGTGAGCTA
ATGATTCTATTTCTGCTGTTTCCAATTCGGTAAGAGCAAAGGATGACGAAAAAGATACTA
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATTCCTTTGAACAATTTCCAGGAAGAAT
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA
TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTTCCTTATTGAAGACGCATTTG
TAATAGCAGAAGTGGATAACGATGTTGATGTTTGGAAATTAGACTAAAGAATTTAGAAG
TATTTACACCTATTGCCAACCTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA
CCTTAAATAACAACATTGCGCCGATTTATCAGATCTTTACATTGTTTCAAGATATAAAT
CTGACGAAAGCACAACTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT
TCAATGAGGACAATATCACTTCGACCTGCCTATTCTTCCCATTATAAAGAATTTTCAA
AAGATGTTGGTAATGGTAGGCACGAGACGAGTACCTTTCTAGGTTTAAATCAATCCTAACA
AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA
CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTGACAGTATACAATCTGTTCTAA
CCACGATAAGCTCAATTCTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT
TACAGATCGATTTTACGAAATGAAGGAAGAAGACAGTTTAAATTGTTGTTTATAACAGTC
TAAAAGCTTTAACCATTAATTTGCGCGTTTGCAGTTTGTGTTTCGTTGATCGAAATTAAT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGTTCTCGACACAATTTTACCTATTTGGTTGAAAAATACTCTATATC
CCGAAAATATTATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTGGAGAAGAAGGCCCA
ATGAATTGAAGATTAAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC
TAGTCGAGGCCAGCTCCTGGACTTTGTTTGAAGAACTCTTTGCTACAGTTTCGGTCTAA
GTTTTGATGAACATGATGACGATGACGAGGATAATGATGATTGACCGGATAATGAAC
TTGATAATAGTTTCAAGATCACTGTGCGGATGCTGAATCTACAATACTATTATCATATTGATT
CTCCATTTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG
AGGGTGAACATAGCAATATAGAAAACCTTAGAACTGTGCTTCTTCACTACAGCCAGCTC
TGATTCTTAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA
ATGAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA
CCAGACGCAGTTTCTCTCGAGTCTTATAGAGAGCGGTAATAACAACCTGTCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTSLRTPNQIIELEKPSTLSPLSRGKKWTEKLARFQR
SSAKKKRFSPISSSTFSFSPKSRVTSSNSSGNEDGNLMNTPSTVSTDYLPQHPHRTSS
LPRPNSNLFHASNSNLSRANEPRAENLSDNIPPKVAPFGYPPIQRTSIKKSFLNASCTLC
DEPISNRRKGEKIIELACGHLHQECLIIISFGTTSKADVRALFPFCTKCKKDTNKAVQCI
PENDELKILISDFLIHKIPDSELSITPQSRFPYPSPLLPPFGLSYTPVERQTIYSQAPS
LNPNLILAAPPKERNQIPQKKSNTYFLHSPGLHRRIPSGANSILADTSVALSANDSISAV
SNSVRAKDDETKTTLPLLRSYFIQILLNFOEELQDWRIDGDYGLLRVLVDKLMISKDGQR
YIQWCWFLFEDAFVIAEVDNDVDVLEIRLKNLEVFPIANLRMTTLEASVLKCTLNKQHC
ADLSDLYIVQNINSDESTTVQKWI SGI LNQDFVFNEDNITSLPILPIIKNFSKDVGNR
HETSTFLGLINPNKVVEVGNVHDNDTVI IRRGFTLNSGECRSRQSTVDSIQSVLTTISSIL
SLKREKPDNLAIILQIDFTKLKEEDSLIVVYNSLKALTIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ
DYRCFTSFGRRRPNELKIKVGVLNVDYSDKIDELVEASSWTFVLETLCYSFGLSFDEHDD
DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVASSVQPALIPNIRFSLHSEEEGTNENENENDMPVLLSDMDKGIDGITRRSSFS

SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTCTTC
AAGATTATCGTGATGCTAATGCTAGAAAGTAATATATATCGCGTCAGGACTCTGTCTCCACAA
CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGCGTGTGCAAAACC
CTGATTTCAGACCCAGAATGATATCCTTCTCTGTAGTTTTGTAGATGTCATATATGTACGT
TTATGGAACAGCATTTTAGAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTCTTTT
CCGTGTACTCGCTACACGTAGAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG
ACGTTTCATTAAGACTCAGTTAAGATTGCCTTGAGAATAAACAAAAGTAATCACAGTTAAC
TATTGAACAAGAGTGCACCTATGACTTCACTTCTTTCACAGCCAGCGTACACGTTGGTTT
TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTCAGAAAGCTCTTGAAA
AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAG
GAAATCCAATGCCTGAATTGTTGATGCACATAAAGATTTGTTCATGCCTTCTAAAAATA
AGGAATTA AAAAAGCTTTTGTACTTCTACTGGGAAATTGTTCCCAAACCTAGCTGAAGATG
GAAATTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC
CTAATGAATATATTAGAGGTAACACATTAAGGTTTTTAACGAAATTGAGAGAGGCCGAAC
TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTT
GTAAGTATGCAATCCTAGCAGTTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTCCCG
ATGCTAAAGAAATCATCAATTCGTTTCATAGTAGCTGAAACTGATCCAATATGTAAAGAA
ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAAATGCCTTACACTATTTAGAGAACA
ATATTGCTGATATAGAAAACCTAGACCCTTTATTACAAGCTGTCTTTGTTCAATTTATCA
GACAAGATGCAAAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC
TGCTTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT
TGTCTGCCAATCCAAATGTCTTGGTTCTGCGGTTAACAAATTGATTGACTTGGCCGTC
AGGTTTCTGATAATAACATTAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA
ATAACGTAGGTGCTTTGGAAGAGTTAACCCTGGATATTTTGAGAGTCTTGAATGCAGAAG
ATTTAGACTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG
CTGAAGATGTTGTTTCACTTTTGAAGAAAGAGCTGCAAAACAACCGTAAATAACCCAGATC
AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACTATTCTGACCGTGGCTGTAA
ACTTTGTAGAAATGGCAGCAAGTGTGTTTCGCTATTATTAGATTTTCATCGGTGATTTAA
ACTCGGTTGCCGCCAGTGGTATCATTGCCTTTATCAAAGAAGTGATCGAAAAATACCCAC
AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA
AAGCTTACC GCGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC
AACATTGTTGGAAGCACATTTCGTAACAGCGTAGGTGAAGTTCCATCCTTCAATCAGAAA
TCAAAAAGTTAACACAAAACCAAGAACACACCGAAGAAAATGAGGTTGACGCTACCGCCA
AGCCAACTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTCGATG
TGAAGACTTCTCAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCGCC
GGTTTGTTTTAAAGTGGTGATTTCTACACAGCTGCCATTCTGGCCAAACCCATCATTAAC
TTGTTTTTAAATTCGAAAACGTTTCCAAGAACAAAACCTGTCATCAATGCTCTAAAGGCGG
AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGGAGAAAA
AAATTGATGAAGATTCTTTAGAGAGAGTTATGACATCTATTTCTATTTTATTGGATGAAG
TTAATCCTGAGGAAAAGAAGGAAGAAGTTAAACTTCTGGAGGTTGCATTCTTGGACACCA
CCAAATCCTCATTCAAGAGACAAATTGAAATTGCAAAGAAGAACAAGCATAAGAGAGCAT
TAAAAGACAGTTGCAAAAACATCGAACCAATTGATACGCCGATTTCTTTTCAGGCAATTTG
CTGGTGTGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTGAAAGCTGAAGAAGATAG
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGATTTACAAAACATCAAT
TTGACGTCGTATTAGATGTTCTTCTTGTAAATCAAACGAAAGAAACATTGAAAACCTAC
ATGTGCAATTTGCAACTCTTGGTGATTGTAAGATTATTGACACACCACAGAAGACCAACG
TGATTCTCATGGCTTCCACAAATTCAGTGTACTGTCAAAGTTTCTCTGCTGACACAG
GTGTCATTTTCGGTAATATTATTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA
TTTTAAACGACGTTTCATGTTGACATTATGGATTATATCAAACCAGCCACTGCTGACGATG
AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAACAAAATATCGGTCAAATCAC
AACTACCAACATATGCATGCTTATTTGAGAGAAGTGGTCAAGGGAACATAATGGGTATT
TAACACCATCAGAGTCGTTGGGAGAAGATGTTGATAGTTCTTAAGTTGTAATCTGTATG
CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACTTGTGTATCGAAAAGGATTTCCAAAA
CCAATGATGTCATAGGTTATGTTTCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGTCTCTCACTCATGTTT

GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPPEL
LMHIIRFVMPSKNKELKKLLYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG
NTLRFLLTKLREAELEQMVPVSLACLEYRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT
PALKAQYIELLMELLSTTTSDDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSNNI
KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
LKKELQTTVNNPDQDKAMQYRQLLIKTIRTVAVNFVEMAASVVSLLLDFIGDLNSVAASG
IIAFIKEYIEKYPQLRANILENMVQTLQKVSRAKAYRGALWIMGEYAEGESEIQHCWKHI
RNSVGEVPILQSEIKKLTQNGEHTEENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS
VTDEERDSRPPIRRFVLSGDFYTAAILANTI I KLVLFENVSKNKTVINALKAEALLILV
SIVRVGQSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLEVAFLDITKSSFKR
QIEIAKKNKHKRALKDSCKNIEPIDTPI SFRQFAGVDSTNVQKDSIEEDLQLAMKGDHAIH
ATSSSSISKLKKIVPLCGFSDPVYAEACITNNQFDVVDVLLVNQTKETLKNLHVQFATL
GDLKIIDTPQKTNVIPHGFKFTVTVKVSSADTGVIFGNIIYDGAHGEDARYVILNDVHV
DIMDYIKPATADDEHFRTMWNFAFEWENKISVKSQPLTLHAYLRELVKGTNMGILTPSESL
GEDDCRFLSCNLYAKSSFGEDALANLCIEKDSKTNDVIGYVRIRSKGQGLALSLGDRVAL
IAKKTNKLALTHV

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AAACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTTT
ACTGCATGTGGATAAAAGTTTTTCGAATCGTTTGCAAGCAAATGTAACTATTACTTTTT
AATGATTTCTGATACTCTTTGATTCCATCTCTGTCATACTTTTTTCTGCATTTGAAACGCT
AATTAAGTATTTCTTGCCCTGCTTCTTTTCTTTTGATTTCTTTTTTTATTCTCAAGTT
TTTAATTTCTGGAGAATCTCTTTTTTTGTTTATTTTGTAAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGATC
TACAGAACCAATATTAACACAATCTTTCTCAAACCTGTAACACCGAGTTTTTTTTTCCCA
CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAACAACAGAATAA
CGAAGAGTGCTAAGGGACAAATGCAAAACCCCTCCGTTGATTCGTCCCGATATGTATAATC
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT
CTCCGCAAATTGCACAGCCCAGCACGTCCCAAAAGTTACCTTATAGAATAAATCCTACAA
CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGATGATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCCCTATACATC
CATCTTATATCATCCTCCGCAATCAAATGAAAGAAATAACATCAAGAATCTCGAACAATAA
CTCAAATGCTCATGTTAGTATTCAACCTTCCGTGGTATTCCCCCTAAAAGTTATTCCA
TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA
CCAGTGTTACTACTGCACCTCCTTCTTTTCAAAACAGTGCTGATACCGCTAAAAATTCAG
CTGATAATAATGATAATAATGATAATGTAACCAAACCTGTTCTGATAAAGACACCCAAC
TCATAAGTAGTTTCAGGCAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACC
CTCAAAAGGCATTTAGACAAAGGAAAGAAATAACATCAAGAATCTCGAACAATAAATCAA
AGATATTTGACGATTTACTAGCAGAAAAATAAACTTCAAATCATTAACGATTCTATTAA
GAAATGACAACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT
TAAGAAGTGAGTATGATGTCTTATGTAACGAAACAACATGTTGAAGAATGAGAATAGTA
TAATAAAAAATGAACACAACATGTCAAGAAATGAAAATGAAAACCTAAAACCTTGAGAATA
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAAATACTAAAAGAAAGG
AACAAGAACAACGAGATGAAATAGAGCACTAAAAAATAAGATCCCTGGAGGAAA
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPPLIRPDMYNQSSSMATYNASEKNLNEHPSQIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNPIQPPLPNLMLHLSGSPDYRSMHQSPIHPSYIIPPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQISISLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKVPDPKDTQLISSGKTLRNTRRAAQNRRTAQKAFRQ
RKEYIKNLKEQSKSIFDILLAENNNFKSLNDSLNRDNNILIAQHEAIRNAITMLRSEYDV
LCNENNMKNLENSIIKNEHNMSRNENENLKLLENKRFHAEYIRMIEDIENTKRKEQEQRDE
IEQLKKKIRSLEEIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAACAACAAACGTCAGGTGGAAAAAGCTGCCGCAAATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAAATCTACACAGTTGCCATATCGTTTATCGCCTTATTCTTCAGAAACATTTCACTCAACTA
CTCTGGTGCATTATTTTCATGTTAGTTACCATATATACCGGCCGCGCCGATCGGGGTTTTT
TGATTGAAAAAATTGGTATATTTTCAGTACACATATAAATAAAACCCCTCAATTTGCCCTCT
CCAACCGTTATAACTATTTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG
GGATTTTTTCCATCTAATAACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCCAGTTTATGATTC
TAACCATCAACGAATTAAAAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA
ACATGTTGAAGGATTATTTGTTTGTGATCTTTTGTACAAAGCTAATAAGTAATTTTTTTTT
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCCA
GAAGATTGTTTCGTTGGTTATTTGGACTCACCATTTTTGAGGGGTACCGTAGAAAAGGAAG
TCACAAAGGTCAAACAATCGATCGAAGACGAACTAATTAGATCGGACTCTCAGTTAATGA
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA
AATTGAACGACTTGATACCACATACCCAATGGAAGGAAGGAAAGGTCTCTGGTGGCGTTT
ACCACGGTGGTGATGATTTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG
CCAATCAATTACATCCCGATGTCCTTCTGCCGTACGTAAAATGGAATCCGAAGTGGTTT
CTATGGTTTAAAGAAATGTTTAAATGCCCCCTCTGATACAGGTTGTGGTACCACAACCTCAG
GTGTTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC
GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAACTGCACATGCTGGGTTTGACAAAG
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG
TGGACCTGGGAAAAGTGAAAAAATTCATCAATAAGAACACAATTTTACTGGTGGTTCCG
CTCCAAACTTTCCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAATAGCACAAA
AATATAAACTTCCTTTACACGTCGACAGTTGTCTAGGTTCCCTTATTGTTTCATTTATGG
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA
TATCATGTGACACTCATAAATATGGATTGTGCACCAAAAGGCTCGTCAGTTATAATGTATA
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT
ATGGCTCTCCTACATTAGCAGGGTCCAGGCCTGGTGTCTATTGTCTAGGTTGTTGGGCCA
CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG
CAATGAAGTTTAAAAAATACATCCAGGAAAAACATTCAGACCTGAATATAATGGGCAACC
CTAGATATTTCAGTCATTTTCATTTCTTCAAAGACCTTGAACATACACGAACTATCTGACA
GGTTGTCCAAGAAAGGCTGGCATTTCATGCCCCACAAAAGCCGGTTGCACTACACATGG
CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACATACCG
TGCAAGAGTTGAAGAGCGAATCAAATTCTAAACCATCCCCAGACGGAAGTAGCGCTCTAT
ATGGTGTGCGCCGGGAGCGTTAAAACTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC
TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPHLLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVTKVKQS
IEDELIRSDSQLMNFPPQLPSNGIPQDDVIEELNKLNDLIPHTQWKEGKVSAGVYHGGDDL
IHLQTIAYEKYCVANQLHPDVFPVRKMESEVSMVLRMFNAPSDTGCGTTTSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPHGIADDIEGLGKIAQKYKLPLHVDSCLSFIVSFMKAGYKN
LPLLDLFRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPWTGGLYGSPTLA
GSRPGAIVVGCWATMVNMGENGYIESCQEIIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNIHELSDRLSKGWHFNALQKPVALHMAFTRLSAHVVDIEDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCTGTGGAGCAGAT
TCCTGTGGAACCTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGTCTGT
TCTTCGACTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
TCAGACATTATCCTTATGGTTTATAGCGTAATTCCTTAATTTTGATTCTTCAAAGTATA
TATATTTAGAAGAGAGGAAATTTTCTCATGTCTTTTAAATCCCTTTGGGTGGCG
AAAAAAAAGAATGTAAAAAATTTGCCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAGTAAATCATTGAATTGTTGAACAAGCATTGACAGATATGATAA

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAGAATAAAGTTACTA
TAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTGCGTCCTCGTATGCCAAG
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATTCATGGTTATGAAGTGAGAAGAA
TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCCTCCAGACAGGAG
CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTTCAGCATTTGCTTTAAAA
CCAACCCCTCCAGATTCCACTGGGGTCCCTCATATTTCTAGAGCATACAACGTTGTGTGGGT
CTGTTAAATATCCAGTTAGGGACCCTTTTTCAAAATGCTAAATAAATCTCTAGCTAATT
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTCCTTTTCCACTACGAACCCTC
AAGATTTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC
AAGAAGATTTTGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGGAGA
GTAACATTGTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAATGCCA
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG
GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA
ATTACCATCCCTCCAATGCAAAAACCTTTCAGTACGGTAACTTGCCATTGGTGGATACGT
TAAAGCAATTAAATGAGCAGTTTCAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT
TAATGCCTATTGATTTAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG
ACACATATGATACCTTTTGTAAAGTACTGGGGAATTTATTAATGGATGGCCATTCTT
CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG
GTGTTGAACCAACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA
TTGAAATATTTAAAGACACTGTAATAATATTTTCAAACCTGTTGGAAACAGAACATC
CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC
AAAAGGCTGACTTTGGACTTCAATTACTCTATTCTATACTACCTGGTTGGACAAAACAAA
TCGATCCTTTTGAGAGCTTGTGTTGAGGACGTTTTCGAAAGATTTAGAGGTGACTTAG
AAACGAAAGGTGATACTTTATTCCAAGATTTAATCCGTAAATATATCGTTCATAAACCTT
GTTTCACGTTTTCATTTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC
AAACAAGACTGAGAGAAAAAATTACTGCCCTTGATGAACAAGACAAGAAAAACATCTTTA
AACGTGGTATACTGTTACAGGAGAAAACAAAATGAAAAAGAAGATTTATCTGTTTACCTA
CCTTACAAATAAAAGACATCCCAAGAGCTTGGTGATAAATATTTCAATCGAACGAGAATA
ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC
TAAATGACATAATAACCTTTGAACTCTTCCCATACTTACCTTTATTTGCTGAATCGTTAA
CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAATTACATA
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCTAACACCACAGAGCCTCGCC
TGATTTTTCGGGTTTGACGGATGGTCTTTAAATTGGAAGACCGACCACATTTTGAATTCT
GGCTAAGATCTTACTAGAACTGATTTCCATAAAAACAGCGATAAATTGAAAGTTCTTTA
TCCGCTTATTAGATCTTCAAACACATCTTCTGTAGCAGATGCCGGTCAAGTTGCTGAA
GGGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCCTCAATGGTA
TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTAGACAATGAAGAACTTTCC
AAAGAGAAGTTGTGACAAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA
TGAATTTTATCACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAGACTTCAG
ATTATCCTCTTATGGATCCAAATGTAACATACTTTGATAAAATTTCTTTCCAGGTCC
ATTACATCCTCCCAAGCTTTATTTGGGTGTGCGGTATACACATAAGGATGGCTCTGCATTC
AAGTTATGTCAAATATGCTAACATTTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG
GTGCTTATGGTGGTGGTGCTTCTTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCCT
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC
AAGTAGACGCACCTAAAAGTCCCAAAGGAGAAGGCGTGACGTATTTTCATGAGCGGTGTTA
CAGACGATATGAAACAAGCAAGAAGGGAACAACCTTAGACGTATCTCTCCTGGACGTTT
ATAGAGTCGCCGAAAATATCTACTAAACAAGAAGGGGTGAGTACGGTCAATTGGACCTG
GAATCGAGGGGAAGACTGTTTCACCAAATTTGGGAGGTGAAGGAACGTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGYEVRRILPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKS LANFMNAMTG
PDYTFPFSTTNPDQFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VYVNEFMKGQISNANYFWSKFQCSIYPSLNSGGDPMKITDLRYGDLDFHDKMHPNSNA
KTFTYGNLPLVDTLKQLNEQFSGYGKRARKDKLLMPIDLKKDIDVKLLGQIDTMLPPEKQ
TKASMTWICGAPQDITYDTFLKVLGNLLMDGHSSVMYQKLI ESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIEQLELSKKDQKADFG

QLLYSILPGWTKIDPFESLLFEDVLQRFGRGDLETGKDTLFQDLIRKYIVHKPCFTFSIQ
GSEEFKSLDDEEQTRLREKITALDEQDKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI
PRAGDKYSIEQKNNTMSRITDTNGITYVRGRLLNDIIPFELFPYLPFAESLTNLGTTT
ESFSEIEDQIKLHTGGISTHVEVTSDPNTTEPRLIFGFDGWSLNSKTDHIFEWSKILLE
TDFHKNSDKLVLIIRLLASSNTSSVADAGHAFARGYSAHYRSSGAINETLNGIEQLQFI
NRLHSLLDNEETFQREVVDKLTTELQKYIVDTNNMNFITSDSDVQAKTVESQISKFMERL
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVPTHKDGSALQVMSNML
TFKHLHREVREKGGAYGGGASYSALAGIFSFSYRDPQPLKSLETFKNSGRYILNDAKWG
VTDLDEAKLTIFQQVDAPKSPKGEVTVFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY
LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACATCGCCCCAGTAAATGCA
TACGCAAGATAAGATAACAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA
TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTTCATCGGTCTC
GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT
GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCATAACAC
ATTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTCAAAGAATATATA
TAATAATGCAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA
AATAAAAAGTAAGCAGGAGAATGAATCGTGTGTTGGTATAGACGTAGATCATATGATAGGGG
TCCTGCTTCTGGCCGTAGTGGTGGTGTGTTTGGGTTGGCGCTTCGTGTTTGACTAATGAAT
TGCTCGAGACAAACGCGTACAATAAACCTTCTTCTTACTTATCTAAACATATCATCGT
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC
AGGAACGGACAGAACGAACATTACCTATTACACACAAGAATCTTTTTTCAGAGTTCCTAC
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG
TGAAGGATACAATGAGGTGAGTCTGCTATTTTGGCTCTTGTGGTTCGTGGCAAAATTTGG
CGGCTAACGCTGCTTTGTCTGATACACAGTGGCTTCGTCAACAATCTTTTCATCGACAT
CCTCATTTTACCTTATTTCTTGCCACTAGTCTAGGAATAGAAACTTTTTCGACAAAAA
AACTGCTGGGGTTATTTGTGTCTTTGTTTGAATTATCTTAATTGTGATGCAATCCTCGA
AGCAACAGGATTCTGTGAGTGCTTCCTCCTTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGTCATTGGGTTACAGTGTCTATACAACCTTTTGAATACGAAATATCATCCAAAGGTC
TCAGACTAGACATTCAGATGTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT
GGCCAATTTTAATAATCCTGGATATAACACATATGGAAACTTTTGAACCTACCAAGTAACT
TCCACATTTCTTTCTTGTCTATGTTAAATTGTATCATTATCTTTGTTAGTGAATTTTTT
GGTGTAAGCCCTCATTTTGACATCACCTTGGTGGTTACCGTTGCCTTAACTTTTACTA
TCCCGTTAGCCATGTTCTGCTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA
TCATTGGTGTATTTTTCATTTTTGTTTCACTTTCTAGTTAACCATCGGGGAGAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTGAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMIGVLLAVVVVFWVGASCLTNELLETNAYNKPFFLTLYLNISFALYLTP
DLWRIIQSRRKSLQERTERTLPIHTQESFSEFLPLLSSTPSTSSNLSSIADTKVKDTMRL
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFSTKKLLGLFV
SLFGIILIVMQSSKQDSVSASSFLVGNLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTLLFWPILIIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALTFTIPLAMFADFVWREAFFTPWYIIGVIFIFVSFFLVNHRGESAVEKDCA
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2:
983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTAGGAACAGCA
GGCATTATATCCAAAACCTTTTTTAAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGTCTGGCAACAAAAAAGTACATTTAATTTCAATGATTAAAAAGACATTAAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAAATATTCTACATGCTGCTTTTAGAAATTTG
AAGCGGCATATGGTGTTTCTTTGCGGAGACGCGCGCTCAGGGGAACTGCGATTCCGAAAG
ATGCCTTTCCGATCCCATATGCCCATCCCAAGATCATGCCCGGGAGAGCAAATGTCGCC
CCAGCCAGGTGCGACACATCTGTCTATTCGACCATAAGTATTGTCAAAGCTAGGGTTAAT
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTTTAAACGTTGAGATACTAGTGAACGTA
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTTCCAACACA

TTTTACGGTATGTTTATTATTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAAA
TATGACAGACAAGAAAGGAAATTCATTCACCTCTTTAATCGTGGCGATTATTCGCTAACG
ACGTGATTAAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG
ATGAACAAATTTATGGTTTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTCGGAGGTAAAGTACCGGGAATGCTTTACAATGAATC
AGCTATTGGCGGATATTGACCAACCAACTAAAAATTTATATCCTGCTCCGATTTTTGT
CTTGGCCGTGAAATCCATTATGCACATTTTACTAACGTTTATCAATAAGTTCGGTTTC
CCGTCTAAATTTTTTTTACGCAGTTTGTGTAACACTAACGTTGACGGTAACATTAAGATCG
TTTACGCTTTGACCACTATCAAGGGTGTGGTTCGTCGTTACTCCAACCTTGGTCTGTAAGA
AGGCTGATGTTGATTTACACAAGAGAGCTGGTGAATTGACCAAGAAGAATTGGAAAGAA
TTGTTCAAATTTATGCAAAACCCAACCTCACTACAAAATCCCAGCTTGGTTCTTGAACCGTC
AAAATGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACAACGTCGAATCCAAAT
TGAGAGATGACTTGGAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGTTTGCCTGTTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQGSFQHILRLNTNVDGNIKIVYALTIIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTHYKI PAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAACTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC
GACAGGTCGATGACTTGTAGGGCTCTTGACAGACTCTTCTCTACGCCAAAATCATTTTTTA
AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC
CACACTGAGGCCGGTGTGATTTGTGTAAACTAAGTGGACTAAGTCCCGTCGCTGTTATT
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCTTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG
AAATAATCTGGTGAACATTTTCTCCATTCTATCTATCACAACAGACTCACACATATATAC
ATGTATATATTTGTAACCTTTGTATATATCTTTTGTGTTTTTGACCTTTTCTCTCTATG
TTTTTTCAGCCATACAAAATATGGGATTTTTAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTTCGGATATGGGAACAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC
AAATCGCCCAGTTAAACTTCCAGCTGCAAAATATTCAAAAGAATTTGCAAAGATCAAACA
ACAAGCAACCCTCGTTAAGAAAACAGGCTTTGAAGATTTTAAATAAACGTAACAGTTAG
AAAATATGAAGGATTCTTTGATTTCTCAATCTTGGTCCATGACGCAAGCCCAGTTAACA
ATGATAACTTACAGAACAATGATCACTATAAACGCCTAAAGCAAAACAACAAATGCCA
TGAAGGCTCAATACGGCAAGATAAATATCGACAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG
AGGATTTCACTTTGCCAACCAGCGAAAACCTATTAGGTAACGATATGCCCAGTTACTTAC
TAGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA
AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVVIGGSQDWLKHYSYKLFKAIMNRIFGYGNKSHDQLLOESNQSMNQA
QQSLSNRISQLDTQIAQLNFQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQSWSMTQAQLTNDNLQNTMITINALKQTNAMKAQYGKINIDKLQDMQDEMLDLIEQG
DELQEVLAMNNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNMPSYLLGANAPP
AFIDEENLDTEDKNKALESQA

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAATCAATTAAAATTCCTTTTCTCTCTACCTTTGCTAATATTAAAAACCATAGTTGT
AAAGGGTACTTAATGCTATATTCCTGTTAAGTTTCCATTTTCACCTTGTTTTTCCAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT
ACCTTTTTTTTGGGTGAAGAGAAGTAGTATTTGTTTTTTCATGGGAGTGGAAGTCCTTTC
AAAATAATCCGAGCAGTAGTGCTGTCTAGGCGGAGATTATTGAAAGTCGGCATGCGCTG
CAGCTAGCGTTTTGTTTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG
AGGGTACGTTGAAACTTTTGCCTTTCCACGTCAGTTTATAATATCAAAGCAGCAATATA

CACATTTAATGGTTTGCCCTTAGTGACTATTAGGGCGTTTTGGTGAAAAGAAAGAGTCGC
TCAAAGAAATCAATATAACCATGGCTAAATTTTTTGAAAGCAGGTAAAGTTGGTACGTAAA
TTTAACAGAGCAAACGCTCTAATTAAGATATCGAATAAAAGGGGACTTTCAGGTGCATAA
GATGGGAAATTGTACAATCTGAGGGACAAACAATATGGAAAGCAGTACATGATTGTATTG
TCATTGTAGGAGGTACCAATTGTGCCAGTAAAAAGAGAGGGCCCGGGAGCACCACATT
CACGACCAATCGTGTTCGATCTGCAAAAAAGGCACATGGAAAATGTAATTTATCAGTGTTT
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTAACTTTCCAGGGAAACAAAAAGCT
AAATCCACTTCTCTTTTATTTCAAATATCATTAGAAATAGAAAAATTTACTAACAAATT
TTCGTATTATCGTAGCTGTTCGTGTTTCGTGGTTCGTACGCTGGTAAGAAGGTTGTGATCG
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTCGGTTCACGCTTTGGTTGCCGGTA
TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTCGCTAAGAGAA
CTAAATCAAGCCATTATCAAAGTCGTCAACTACAACCACTTATTGCCAACCAGATACA
CCTTGGATGTTGAAGCTTTCAAGAGCGTTGTATCTACAGAGACTTTTGAACAACCATCCC
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAAGACATCAAGCTGGTA
AAAACCAATGGTTCTTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVRGRYAGKKVIVKPHDEGSKSHPFGLHALVAGIERYPKVTKKHGAK
KVAKRTKIKPFIKVVNHNLLPTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAACT
AGGGCTAATAAAGAGGTAACGGTCGGTTCTCTACTAAGGTTTCGTATTGTGTGGCACCGAT
GTTAAGCACTTTTAAGCGGAATAACTCGAGTGGAATTTTATGTTTAGTTAGGTTTTACC
TTGAATTTTTTTAAAAAAGAGTCAGACAGGCTCGCTCTTTCTACTAAATATTAGG
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCAAAATTTAT
CTTACAAAGAGCTATTAGTATCTTGGTTCTTCTATTTTCTTCGATTATTGGTGATTTTTT
CCGCCTCTAGCCAAATCCGAGCGTTCATCGATTTTTTGGGGAAAACAGCACATGCAATA
AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAATCT
TTTGCATATTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTTCTTCAGATGACG
ATGATGATATTTCTTTTGAATTAGGCACCAGGCCTCCAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCATTACAAACACAAATTTCCCACTACTTTGGAGGTTACAACGACCACATTAA
ACAATAACAGAGTAAAAATGATAACCACTGGTTAACCAACTGAATAAAGCTCAAGGTG
AAGCAAGCATGCTTCGTGATAAAAAATAAATTTTGAACATTGAAAGGGAAAAGGAAAAGA
ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAACAAGAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAATCGAAAAGGGAAAGTTATTACGAATGTAAAACCAACCGTCAACAACATTATCAACAA
ACACAAACACTATAACGCCAGATTCGTCTCAGTTGCAATCGAAGCAAAACCTCAATCAC
CACAATCAAAAAACGTAAGATAAGTGATAATTTACTGAAAAAATATGGTTCCCTTAA
ACCCAATAGGATTATTCCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCATC
AAATAATAGGCGCTGACCTGAGCACAAATAGAAATATTAAATAGATTGAAGCTTGACTACA
TCACAGAGTTTAAATTTAAGAATTTTCGTCAATTGCTAAAGGAGCCCCCATAGGGGAAGTCCA
TAGTTTCTCTACTTTTTCGATGTAAAAAGACGTTGACCCTCGACAGGTTTCATAGATACTT
TGCTAGAGGATATAGCTGTTTTGATCAAGGAAATATCAGTTCATCCAAATGAATCGAAAT
TAGCTGTCCCATTTCTCGTTGCATTGATGTATCAGATTGTACAATTTCTGCTCTAGTGCCA
CTCATAATTTAGCACTGAAGGATTGTTTTCTTTTATTTGCGATTTAATAAGAATCTATC
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCCTCAGA
TTTTCCAATATGAACTGATAGACTATTTGATAATTTTCGTATTCTTTGATCTCCTAGAAG
GTATATTAAGGGTACTGCAGTCGCATCCTAAGCAAACCTTATATGGAATTTTTTGATGAAA
ATATTCTAAAATCATTTGAATTTGTCTACAACTAGCACTAACCATTTTCATACAAGCCAA
TGGTAAATGTAATATTTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATATAATGAAA
ATGTGGATACATAACTCTTCATATGTGCAAGTACCATGACTTTTTTGGGTAAATCCGAA
ATATAGGTGATAATGAATTGGGAGGATGATATCAAAGCTGATTTATACTGACCGATTGC
AAAGTGTTCCCAAGGGTAATTTCTAAAAGAGGATATTGGGATGGATAGCGACAAATTCCTG
CCCCTATAATAGGTTACAAGATGGAATAATGGCTTTTTGAAAGTTAAAAGATGAAGTTTTAA
ATATTTTGAATAATTTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA
TGCTCATCCACTCCTCTAAATTCCTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

TGGGACAAGACTCCCCGAACTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAAGACCATTTCAAACAATTGCGTGAAGAACAAATCAAGCAGG
TAGAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCCTTGTAGGATTTACCAGAAATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTCTTGTAGTCAAAATCATTCGATCTAACCA
CACTAGAGGAGGCCGATTTCATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)

MRRETVEGFSSDDDDILLELGTRPPRFTQIPSSAALQTQIPTTLEVTTTTLNNKQSKN
DNQLVNQLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELOVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTTLSTNTNTITPDSSSVAIEAKPQSPQSKKRK
ISDNLLKKNMVPLNPNRIIPDETSFLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIVSLLLRCCKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPIHESNMNLHVEPQIFQYELI
DYLIISYSFDLLEGILRVLQSHPKQTYMEFFDENILKSFEFVYKLALTI SYKPMVNVI FS
AVEVNIITSII LNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTTL
HMSKYHDFGLIRNIGDNEGLISKLIYDRLQSVPRVISEDIGMDSDKFTAPIIGYK
MEKWLLKLKDEVLNIFENLLMIYGDDATIVNGEMLIHSSKFLSREQALMIERYVQDPSN
LDLRCHLIEHTLTIIYRLWKDHPKQLREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYVEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFQEM
ARTILESXSFDLTTLEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTCATCACATAAATGCATTCCCT
ACTATTACTAACTTGAACCTTCACTTCACTGGAAGAACTGGGTATTCAAGGTAAAGAAAT
CATTTGTTTTGCGCCAAGTTTCGTCTGACAAGAAATTTTTATTATTATTTCCCACTTTTC
ATCGAAGGAAACGCGTCAAATCCATTCGTTACTACGCGCAATCTGCGTTATTTCTTTTTT
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCTTTTTGATGTTAAATTAA
AAGCGACTGAATGAAGTGCACACATTTTTATTCTTCTTGATTTTCTTTTCTATTTTGT
TTTGCTTTCTCTTCTGTGCGACAACGCTCAACTGTACTCACCATTAGTATTCTCGAAGGC
TTTAGCAGACTTGTGAATAATTAATTGCCCACTTTGATCAAGAAAGATATTTCGCAGCACA
ATACAATAATAACATTCAAAATGGCAATCAATGGTAACAGTATTCCTGCCATAAAGGATA
ATACCATCGGTCCATGGAACTAGGTGAAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC
AGCTTGCTCGTAATGGATCCACAGGACAAGAGGCGGCAGTTAAGGTAATATCAAAAGCAG
TATTCAATACCGGTAATGTGACGGTACTTCGATTGTTGGCTCCACCACCCAGATGCTC
TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCAAATGTGT
TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAAATACGCGG
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCTCTGCCAGAGCATGAAGCTA
TCAGGTTTTTTTAGACAAAATTATTATTGGTGTGTCGTACTGTCATGCGTTGGGTATTGTCC
ATCGTGATCTAAAACCGGAAATCTATTATTAGATCATAAATATAACATCAAGATTGCAG
ATTTTGGTATGGCTGCTTTGGAAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC
CACATTATGCTGCACCAGAAATTGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG
TGTGGTCATGCGGTGTGATCCTATTCGCCCTTCTTACTGGTTCGGTTACCCTTTGACGAGG
AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCTT
CTGATGATGAAATTTTCGCGTGAAGCTCAGGATTTGATTAGAAAAATCTTAAACCGTTGATC
CTGAAAAGCAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAATATCCAA
GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT
TATCAGAAAGTAATTCTTCTATTGACGCTACGATTTTGCAAAAATTTAGTAATATTATGGC
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCCTGGCGCTAATGCAGAAA
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAGC
AACAGCAAGTTAAGAAGAGGCAGTCAATTAGTAGCGTTTCTGTTTCCCCATCTAAAAAAG
TATCGACAACCTCACACGCAGAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC
GTAAAAAGCCAATATCCTTCAACAAATTCAGTGCCTCCAGTGCCTCCTCCAGCAATCTAA
CTACACCCGGTTCTTCAAAACGCCTTTCAAAAACCTTCTCTTCAAGAAGAAATTATCTA
CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA
ATGTGGAAAAGAATCAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAAAGAT
CTTCTAGATCTATCAAGAGAATGTCAATTGATACCAAGCATGAAACGTGAATCGGTGACAA
CAAAATTAATGTCAACATATGCGAAATTGGCAGAGGATGACGATTGGGAATACATTGAGA

AGGAAACAAAGAGAACGAGCTCAAATTTTGCAACTTTGATAGATGAAATTTTGTAGTACG
AAAAGTACGAACAAATAAGGAAAGAGAAGGAAGAGCTAGAACGTAAAGTGAGAGAAGCAA
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA
AATTACTAGAAAAGGAAGATCTGAAAAGAAAACAGGAGGAACTCAAGAAGCAAATTGAAA
TTGATATAAGTGATCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAACTGGATGGTA
ATATTAGATCTATCTCTGCTCCTATGGAAAAATGAAGAGAAAAATATCAATCATTGGGAGG
TTGATATTGACAATATTCTCCGTCGCCGCAACTTTTCTTTACAACTAGACCTGTGTCAA

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAACCTGAGGAAGTAAGTCCAGTGGAACCAA
AGAGAACAGAAAATGAAAAGACTTACAACAGAAAAGAAAATTTTAGAACTATCAGAAGAT
CAAAATTCCTGGGTTTCATCATTAAATATCGATAAAGAGTTGAAATTGCTTAAATGGAAT
ATCCAAGTATAATTGCACCACAAAGATTGTGAGAGGAGCGAGTGGTGTGAGATTCTAATG
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA
GTACCGCAACAACCTGCTCCCGTCTCTGATGGTGGTGGAGGATCTCTGAAATTAGAG
TACCACAATTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAAGGCTATCTGTCC
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTGGTTGATATTTTGAAAAACGGTA
ACCTTGATGTCAATAACCAACAAAGCCAAAGAATTCCAACACCAAGAAGTGCGGATGATT
CAGAAATTTCTTTTGAACCTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTTGAACG
ATGAGAGATTGTACGATGTCCGTGATTCCTACTATCAAAGACAAATCCGCGTTAAAGCTGA
ACTTTGCAGATCGTTTAAATGGATCGAACGAGCGAAACAACTGATACTTACATCTTC
CGATCCTTTCCTCCGCTTAATGGTGACAATGAATTCGCTAAACAGAATAGCCAAAGGGTG
ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG
AAAAGGAAGAAGAAAATGAGGAAAAGGAAGAGAAAAGCCAGAACAACACAAACAAGAAG
AGGATCAAGAAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG
TGCAAAAAATTAGGGAAAAAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAAGATCACT
TAAAAGAGCATAAGCAGGATAAAAAATACAGCAATTGGAATGGTTCTTCTTTAGAAAAT
TCTCAAAATCTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT
TTAATGGTTTGAAGAAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAAT
CGCACCCCAACAATCTGACCTTAACGGGTAACTATCGAGTGATAATATATTCTCACTAC
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA
AGAAAGTTTCTGTTTCATTCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC
TGAATAAGGAAGGCGTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINGNSIPAIDNTIGPWKLGETLGLGSTGKVQLARNGSTGQEA AVKVISKAVFNTGNV
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
LLVERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL
ETEGKLETSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLQKYPsirDSKS
IRGLPREDTYELTPLSESNSSIDATILQNLVILWHGRDPEGIKEKLREPANAETLYALL
YRFKCDTQKLIKQOVKKRQSISSVSVPSSKVVSTTPQRRRNRESLISVTSRRKKPISF
NKFTASSASSNLTPGSSKRLSKNFSSKKLSTIVNQSSPTPASRNKRASVINVEKNQK
RASIFSTTKKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS
SNFATLIDEIFEYEKYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED
LKRKQEEELKKQIEIDISDLEQELSKHKEEKLDGNIRSIAPMENEKKNINHLEVDIDNIL
RRRNFSLQTRPVSRLDPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNVSQLKDSTATAP
VSDGRLRKISEIRVPQFTRKSRHFSSESNKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ
QSQRIPTPRSADDSEFLFETVNEEAETGNSSNDERLYDVGDSTIKDKSALKLNADFDRFN
GSNEAKQTDNLHLPILPPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSHTKEEENE
EKEEKKPEQHKQEEDEKREKVDDMEPPLNKSQKIREKNAGSQAKDHSKDHLKEHKQD
KNTAIGNSGFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNLTL
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKVSGSFKAVKKLVNEVENVLNKEGVL
QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGACTACCGCTTCGTATGCTTTCTTGCACTTTGTG
GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAAACCTATATACTAGGCAAATTACT
AGTAAATGCAGTATTCATATGCTCCTCAAACCGTTTTTTGCAGTATGTTATTGATCCATCG
AATCAAAATTTTTTCACCGCCAAGAGAAAAAAGATCTTACTATTTTGTGCTTATGAAAAA

TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAATTGGC
ACATCCTTGGTTGACACTTGTCTATTTATTAAAAGGTTTTAAAAGTAGTGTTCAGCAGT
TCTATCATATTTTTTTATTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCCCAAAATATAACCAAGATAAAGAAAATCA
ATCATAAAGTGAATTCAAAAATGTCATCGCAAAACCTCAATGATAATCCAAAAAATACAT
CCTCAGCAGCTGAAGATAAGAAGAAACAAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTCGGGGTCAATTAAATTAA
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA
CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTCCTAAGACTAATAAAAAAATGAAAAAGC
GTGGCAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
ACATACATTTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAAACA
ACAATTCAAACCAACGGTAGACAATCAAGAAATTATCAAAACAGGAATGGCAAACAAAGAT
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAATAATT
ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAAGAA
ATAGCTATAACAACCTGTCATACTTCCGTCAACAGCAGTATTATAATAACATCAACTATC
AACAACAATTGCAAACACCATATTATTACTCAATGGAACCTATTTTTAAATCTATCGAAA
GTATCAAAAACCAAATTGAATTCTATTTTAGTGAAGAGAACTTGAAAACAGATGAATTTT
TAAGATCTAAATTCAAAAAGCCAATGACGGATTATCCCCATGAGTTTGATAGGGAAAT
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
GAGAAGTTTTACAACATAAAGAAACAAACCATTTGGAAATTGCCCTTGGAAGCATAGAAG
GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACCTATTTTATTAGGCGG
AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA
AATACAACATTGAGAACTATTGGGACCGAACGATTTAGACAATTATTCTTATATGGGCT
ATCCAAACTTCTTTCCAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG
AAATTAGCAGGCAGTTTGAACAAAACCTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLNDNPKNTSSAAEDKKKQTSCLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTSNTKWTPITPSVIIISGSKDTNSKSGKNSKNSKTNKMKKRKGKYNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRITNNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNSNRNSYKQLS
YFRQQYYNNINYYQQQLQTPYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKFKK
ANDGFIPMSLIGKFYRMVNLSLGGDPNLILASMREVLFQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDETEKYNIEKLLGPNLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCTGTTCTGTTCCCTGTTCCAGTAGAATCTGAGACGGC
TTTTGTGCCATCAGCATTCACAGCACCACCGGTGCCAACAAAGAAGAAATCAAAAAATAA
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTAATGAAGGCAGAGATAAGTCATC
TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC
CTCTGATTAACCTTCCCTGGTTAGTCTTTTGGTTTTGTTTCATAGCAAAATTAAATATATA
TATATAAGCTTGCTTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA
CCGAGACTTTTTTCAAAGGCACGCGTGTCTTTTTTGTGAAGACAATAGATATTTTAGC
ATTGAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT
TTTGCTGTTTGTCTTCTTTCACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG
ATTTACTCGTTCTAACAGAGAAGAAATTTAAATCATTCATCGAATCTCATCCGTTAGTCC
TCGTCGAGTTTTTTGCTCCATGGTGTTCGATTCTCAGATCTTACGCCCTCACTTAGAAG
AGGCCGCTCTATTTTAAAGGAGCATAACGTCCCAGTTGTTCAAATTGATTGTGAGGCTA
ACAGTATGGTTTGCCTGCAACAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA
ATGGTCGTATTTTTGATGGTCAAGTCTATCGCGGTGTCAGATCACCGATGAAATCACTC
AGTACATGATCAGCTATACGAGGCTTCTGTGATTTATTTAAATTCCGAAGATGAAATCC
AACCATACCTTGGAATAATGCAACTTTACCAAGTAGTAATAAACAGAGGCTTGACAGGCTGA
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTATCCCTTC
TAGATTCAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATTCTGT
TTGATGGAATGTAGACTCTTTGGTCGGAAATTCCGTTGCTCTAACTCAGTGGTTAAAG

TGGTAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA
GCAATTTGCCGTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG
ATCTTTTTCACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTCATTGCATTAAACT
CTACAATGTTCCACACCCAGTTAGATTCCCTAAATATGAGAGAACAGTTCCCATTTATTTG
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT
ACGCGAAATTAGAAAAACCACAACCACTAGACAGAGATATGATCGTTGAGTTGGTAAAAG
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA
AGTCCAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA
AGGATGTCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTGCGCCCTA
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA
TCGCCGAAGTAGATTACAGGGGCAAATGATATCTTAAGTTTTCCTGTGACAGGATATCCAA
CCATTGCTTTGTATCCTGCGGAAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA
ATTTGGAAGATGTTTTCGAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTTRFISAIVSFCLFASFLLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNPVVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLDSEDKSLSIHLPNTTEPILFDGNVDSL VGNSVALTQWLKVVLIPYF
TDIEPDLFPKYISSNLPLAYFFYTSEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMRQFPLFAIHNMINNLKYGLPQLPEEEYAKLEKPOPLDRDMIVQLVKDYREGTA
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYATWCIHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFVPTGYPTIALYPAGNNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTTCTGTGACAGGATATCCAACCATTGCTTTGTATCCT
GCCGGAAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTT
GAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGGCAATTTATGATAAATTG
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA
ATAAATAAGCATATATAATGCACATTTTAAACATCTGATTACTCGCATCGTTTCTGGAA
GAAAATAGCTAATATTCTGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA
TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA
CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTTCGTTTTCATCACATTCTAG
TTTACAGTAATTGAGTCTCGATGATGTTTAAATATTTACCTTTTCGTCACTTTTTTTTCCA
CCATTCTTGCAGGTTCCCTGTCAGATTTGGAATCGGTATTATCAAGAGAATACCGGTAG
AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTTATTATACAGGATCTT
TATTAGAATCGGGAACGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AACTTGGCGTTGGCAGAGTAATTAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG
GCGAAAAAAGAAAGCTGCAAATTCGAAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCTCAG
GCGTCATTCTCCTCAAGTGCTGATTTGGTGTTTGATGTGCAATTGGTAGACGTGAAATCAG
CCGCCTAG

YDR519W, 136 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGI IKRIPVEDCLIKAMPGDVKVHYTGSLLES GTV
FDSSYSRGSPIAFELGVGRVIKWDQGVAGMCMVGEKRLQIPSSLAYGERGVPGVIPP SA
DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTCGAATGCCATCGTATTGTACTCAATGGTGAACTTACCACCAT
ATTGTTAAAAGCTATTATTTATGATTTTTACTTACCAAACATTGAAAGGAGACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTTCTAACGCA
TGCATCCTGAGCAATGAAATCATGCAACCTAACATTTGAGGTTAATATATGAGAATTAAC
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAATTATCGATGCAAGGAAAAATG
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAATATCATAT
ACTTTTCGCTTCTATCTCGATGCGTTATTACAAGAAAAATAGTTTACTAACAAATTAACA
AAAATTAATAATAGTGTAATAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA

CTGGTGCTAAACGTGCTCAATTCAGAAAGAAGAGAAAGTTCTGAATTAGGTCGTCAACCAG
CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTCAGAACTAGAGGTGGTAACAAGA
AATACAGAGCTCTAAGAATTGAAACCGGTAACTTTTCTTGGGCTTCTGAAGGTATCTCCA
AGAAGACCAGAATTGCTGGTGTGTTTACCATCCATCCAACAATGAATTGGTTAGAACTA
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTAGACAATGGTTTCG
AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTGTTG
CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT
CTTCCGTTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAG
GTCAATCCGGTAGATGTGATGGTTACATCTTGAAGGTGAAGAATTAGCTTTCTACCTAA
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRKFFELGRQPANTKIGAKRIHSVTRTRGGNKKYRALRI
ETGNFSWASEGISKKTRIAGVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYGQT
LGKKKNVKEEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)

ACCCTATATGGGAGGACAACCTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG
TAGAAGCGGAAAGAGAAGGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT
GGATTTCGAGACATCGTTGGCATTTGGGCCCTCGAATTAAATCTTTTGGCCTGAAAAG
AGATCCATGACGGATGGGGCCGGGGCAATACTATGGTTCGAGCGGTGGCCAGTCTGGAAG
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT
TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA
GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA
ACATAAGAACGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC
GTCAGCAGCAGCAGACCAGCGTGGATGTGGAGCTGCTGCACACGATGTAGCGCGAGCCG
CTGCGCTTGCCCATGCCGACACTATAGCATAACATGTGGTATCAGCATGTGATGCCACGCC
GGTTGCCAGTAGAGGGCCGCTGCTATGTGAAATGGCTGGCGTAGCATTGTACCAGGACA
GGCTCTTCTTACCCGCGCAGTTCTTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA
CCAGCCCAGAAGATGAACTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGGAAGGTATTCTTGCAGGAGA
TGGAATACGTAACAGGCGAGCCGCTAAGGCTGCGCGACTTCCCGCAAATGACCAAGG
CTATGGGCATAGCATTTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTGGAC
GACAGCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCTTT
GGCATGTTCCCGGCCAGCGCAGGCGCGACGTGTGCTGGCGGAGTTCCGTCAAAGTTATC
GCGGGCTGCCGCTGCTGGATGCCGAAC TAGTGATAAAGAGAAGAGGATTTGAAATCAACA
CATAA

YER153C, 254 aa (SEQ ID NO 82)

MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQOOTSVDVELLHTMLARAAALAHAD
TIAYMWYQHVMPPRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNRDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPQPPLRLRDFPQMTKAMGIALM
QQDEQAAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD
AELVIKRRGFEINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)

GGACTAGAAGCCAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC
TGTTAAGGGGATATGTTGCAACTTGACGGGGCGGCACAAAATAACATAGAAACGTAGTA
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAAACCATTGACGTAGAAAT
TGAAAGAAGGAAAGGTATACGCAAGCATTAAACAAACCACAAACACAGACCAGAAGCAC
TCTAGACGGAGAGTAAC TAGATCTACAGCCCCTGGAATCGTTTGGTCAACTTTGAGGT
TCCGGTCGTCCCCCTCTTGATCTGAAAGGTCTTTCTCTAAATCTATATTAACGTATAA
ATAGGACGGTGAATTGCGTTCTACTTCTCAATTGCGTTTGATCTTATTTAATCTCTCTC
TAATATATAGAAAAAAAACCATCTGATTATTCGATAATCTCAAACAAACAACCTCAAAAC
AAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTCCGGTGAAAAAGCTT
CTGAAGCTTTGAAGCCAGACTCTCAAAGTCATACGCTGAACAAGGTAAGGAATACATCA
CTGACAAGGCCGACAAGGTGCTGGTAAGGTTCAACCAGAAGACAACAAGGGTGTCTTCC

AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG
AATATGTTTCCGGTCGTGTCCACGGTGAAGAAGACCCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGKEKASEALKPDSQKSYAEQKEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNAEQGESLADQARDYMGAAKSKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCTTTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCT
TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTTCGGCCTTGTTCAGTGATGTATTCTT
TACCTTGTTTCAGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC
CGAATCCTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTTTGTGTTTGTGAGTTGT
TTGTTTGAGATTATCGAATAATCAGATGGTTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTTA
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCTTCTGGTC
TGTGTTGTGGTTGTATTAATGCTTGCATACCTTTCCCTTCTTTCAATTTCTACGTCA
ATGGGTTTTTTTCCCTTCCCTTTTCCCTTTTCCCTTTTCCCTTCTTTCCCTTCTTTTCT
ATGTTATTTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT
ATTCTAGTCTTGCTATTTTTTACCGCCTCTGGCTTTTGGCTTCTAGTCCCTTGTCCCAAGAG
CCAAGGGCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC
CCTTTTTTTTCCATTTTTCGGCTGGGCGGTTAGTGGGATCCGCCCGCTCCCGGAGATTTTCA
CTTGGAATTTGCGCGTCCCCCTTTTTTTCTTCAATCTCTGACTCCCCCTACCTTCTCCCACT
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAGAACTCCGAAAAATACCGAACAAG
AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPLLRFYVILCRPLQVATYPLNRCQQYSSLAIF
TASGFWLLVLVPRAKGPSTRRHICYRQLAPTHHRPFFSIFGWAVSGIRPLPEIFTWICASP
FFLHSLTPPTFSHFVSVYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCTTCCGTACGTCACAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTTCGTACCATTTATCTTGTGCGGTGTTTTTATTTAAAC
AATAGAAGCTCGCCTAAAGGGGAAATTTTCGATATAAAAATTCAAAAAATGGCTTTCATG
GATCGAGTATTTGTTTGTGCGAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCTCTCGGA
AGAGTTCAAGCTTACCGGGTAAATCAGTTGTGATGCGGTATATTCTCTATACGGCTAATA
GATGAATCAGGGTGTTTTTAAAGTGCATATAAACCTTTTGTCTATTTTTCGTTTATATAAT
GGCGTTGATAAAGAGCCAATATCTATTGTTGTACATAGAGGCAGCTCTCTTAGCAAAAT
AAAAATACAAAAAGTTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC
TGCTTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCCTC
CAAACGAGGCCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTATCGATTAACGAACCCA
TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCAGGACGCTAGTTCTTTCGTGTTGTCTTCATCGCCGCCAAAGATCAGAAAGT
ACAACAAAGTTTTTTATAATTACGCATGGGATAATGTTAACTCAAGGAGTATCTGAGTG
GTTTAAGAGGGCAATCTGGCCTTTCGGGCGAGTAGCTCATCAAGTAATATCTTGGGCACCTC
GCCAAAGAGCTCAGTCCACAAGTTCCCTTGAAGTCTTTAAAGGGGTCTCTCACCCTCTT
CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTTCGT
TACCAGAGAGCGTAGAATCTTTGCCAAATGCTTTCGTGACATATAGCATGGAATCCGTTA
TTGAACGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA
CCATTTACCCGCGCAGTGGAGTTATCAGAACTGTTTGTGTAGATAACTCAGTGGCCCCG
ACAAAGTGGATTATCTATTTTCAGTATCCCAACAAAGCCGTAGCTATTGGTTTCAGCCACC
CTATAAATATTTCCATTGTACCTCTTTCGAAAGGTTTGAAATTTGGGCTCAATCAAAGTCG
TATTATTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA
ATGGTTGCTTTGTAAATAACCCCTTTTTTTCAGCCTGATCATTCATTCCAAGACAAGTGGG

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACCTGTGTGCAAGATTGTGATG
TCCGCTCTAACATTAAAGTTTCGCCATAAGCTCAAATTTTTCATCATCCTAATTAACCCAG
ATGGTCATAAATCTGAGTTAAGAGCGTCCTTACCGATTCAACTTTTATTTTACCATTG
TGGCACTTTCAATAAAACCATTTGTCATCCTCGAATTTGTATTTCGCTTTTATAGCACCAC
ACCAGAAAGACGAAAACCTCATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCTTACCA
TTTCAGACTTGATGACGCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG
GTTCTTTTCACTCGCACGGCTGTGGAACGCTGTGGAACATGTACTCCTTTGGGAAGCGAAT
GTTTCGACTGTGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA
GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCACGGAGAGAATCTTAC
CTCAGAGTGCTCTTGGTCCCAATAGTTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTGAGCCCATGAAGTGTTACCAGTGC
CCTCGGGCTTAAATTATCCAGAGACTCAAACCTGAACAAGGTTCCATCGTATGGCAAGG
CAATGAAATATGATATCATTGGTGAGGACCTTCCTCCTTCTTACCCTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCAGGAACCTTTCGACAACATTGTTCAT
CTTCTATACCAACTAGCTTTTATTCCTCTAGTTTTATGAGTAGCACTGCTTCCCTATTT
CCATAATTAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACTTAATGAGT
TAACATTCGAAAACCTTCGAATAACCCATCCAGTAAATAGTATGAAAAGGTCACCAACAAGAC
GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTTCTATCAAAGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPNEAPSVLLSGCIVLSINEPMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLSPPKIRKYNKVFNAYWDNVNLKEYLSGLRGQSG
LAGSSSSNILGTRQRAQSTSSLKSLKGSSSPSSCTLDKGNYDFPFSAILPGSLPESVES
LPNCFVTYSMESVIERSKNYSDLICRKNIRVLRTISPAAVELSETVCVDNSWPKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVLFENYQYCDPFPFVISENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNCVQDCDVRNLIK
RHKLKFFIILINPDGHKSELRASLPILQFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEYLFSRSASVTGLELLADMRSAGSVPTISDLMTPPNYEMHVYDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQQDLEDLRLTKIRNQRDNLGLPPSASSAAASRSLPPL
NVPAPEDGTERILPQSALGPNSSGVSVPVLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLNKVPSYGYKAMKYDIIGEDLPPSYPCAIQNVQPRKPSRVHSRNSSTLSSSIPTSF
HSSSFMSSTASPIIINGSRSSSSGVSNTLNLELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCACTAAATAGGATTGTGGGGACAAATATGGAA
TGGATCAAAACGTTCTTAGGATTGTGGTGGTAAAACCTGTAAAATCCAAGCTGAGATCTT
AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAGAAGAGACTATATTCT
CAAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCCTG
GATTTACCTTGGCATTCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA
TGATATCACAAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA
AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC
GAAAAAAACATATTACAATCATGTGCGGTGCTGCTGCATCTGCTGCTGGTTATGACA
GGCACATCACTATCTTTTCCCCGAGGGTCTGTTTATATCAAGTAGAATATGCCTTTAAAG
CGACTAATCAAACATAAACTCACTAGCGGTCAGAGGTAAAGATTGTACAGTGGTGA
TAAGTCAGAAAAGGTCCCTGATAAACTGTTGGATCCAACTACTGTTTCGTATATTTTTT
GTATTTCAAGAACAAATTGGTATGGTAGTGAACCGACCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAGGCTGAGGCTGCAGAAATCCGTTATAAAATATGGTTATGATATGCCAT
CGGATGTATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA
TGAGACCATAGGTGTTTATACACTACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA
TTTACAAAACCTGACCCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA
AACAAACAGGAGATCACAAACAACTTAGAAAACCATTTCAAAAAGAGTAAAATCGACCATA

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTGCTACAAAGGACAAATTCT
TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)

MSGAAAAAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVNNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKR
MANLSQIYTORAYMRPLGVILTFVSVDEELGPSIYKTDPAGYVVGKATATGPKQQEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVG VATKDKFFTL SAEN
IEERLVAIAEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT
TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG
AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTC
GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGCTTCATTAC
ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG
AACCTAGTAAAATGAATTCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC
TACAATTTTGGCAACGCCTGAACAACCATGCGGATTACCATTATTTATATTGACAAAGATG
GCTACCTATGAAAAGCATAGACTTACTAACAATTTTTTTTTTCAAATATGTTTGAAAAACG
TGGATTAATATAGTGATAAAATGAAGGTGAAATCGATTCTTTTTTCAGGTGCCAAAATCT
ACCCAGGCAGAGGTACCTTGTGTGTCGGTGGTGACTCCAAAATCTTCAGATTCCAAAAC
TCCAAATCTGCCTCTTTGTTCAGCAAAGAAAGAACC CAAGAAGAAATCGCTTGGACTGTCT
TATTCAGAAAGCATCACAAGAAGGGTATCACCGAAGAAGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA
GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAGAAAGAAATGAAGGCCAACAAAG
AAAAGAAGAAGGCTGAAAAGGCTGCTAGAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLFKQRKNPRRIAWTVLFRKHHK
KGITEEVAKKRSRKT VKAQRPITGASLDLIKERRSLKPEVRKANREEK LKANKEKKKA EK
AARKAEKAKSAGTQSSKFSKQQA KGAFAQKVAATSR

YGL032C, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCATATTTTTTTTATTACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTTTCA
GGATTACATTTCGCACAATAGAATAAATGACTAATTTTCAAGAATTGTTTTCAACCTGCCG
GCATTCAAGTTATTATAAGTTATTGTTTGATGGTAAAACTTCGCCATCACCGGTTGCTGCG
TTTATTGCAAAATTACTGAAACCATGTAATTTCCGAATACGGTAATTACACGCAGTTTGA
AATTGACATGCAAGTTTAAACAAAAAACTTCTGTCCGCATCTAAAGCTTAATTAAGGGA
CTGTTTCATACCTTCAGATCCAAATATACTGAATATCAGGCAATTGATTTCCCTTGTAAT
ATACAATATAAATAGTTGTAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTATTCC
TCATTCTAGAATGATTGTAAGCTCTCAACAGTCACTTGTGTGCCAAAATATTATACCTAC
TTCATACATTTTCAATTAAGATGCAGTTACTTCGCTGTTTTTCAATATTTTCTGTTATTG
CTTCAGTTTTTAGCACAGGAAGTGAACACTATATGCGAGCAAATCCCTCACCACCTTTAG
AATCGACGCCGTACTCTTTGTCAACGACTACTATTTTGGCCAACGGGAAGGCAATGCAAG
GAGTTTTTGAATATTACAAATCAGTAACGTTTGTGAGTAATTGCGGTTCTCACCCCTCAA
CAACTAGCAAAGGCAGCCCCATAAACACACAGTATGTTTTTTTGA

YGL032C, 87 aa (SEQ ID NO 94)

MQLLRCSFISVIA SVLAQELTICEQIPSP TLESTPYSLS TTTILANGKAMQGVFEYYK
SVTFVSNCGSH PSTTSK GSPINTQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCGGGATGGTGGGTTGTTCTGTACCCCCGATTACACCGCTCTGCCTATTCATTTTATC
GTTTTCGTCTTTTCTTTCAATGTATTGATAATTAACGTGTCTATGTGATGCTATTGGTAT
ATAGCCTTTCTTGATATATCCCTCTAACAATTATTACAAGTGTTTCTGTTTAAAGCAAGTG
CTAGAAGTGACTCGGTTCTCTTAGGAAATCTAAACGCAAGATTTCTCTTATGGTGATTG
TAACAATTATGAGATACTTCACTAGCCACCTTAACCTTACGGACCTTCTTTTGAAACGA

TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTTCATTATAGGGAAATTTT
CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTCACAGTGTAGTCAG
TCCGCATAAGAGCATTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG
AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCTTGGATAAAGAAT
TCGTCCCCACTGAAAAGTTACTGAGAGAAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
AAAAATCCACTAATGTAGAGATCAGCAAACTCGTGAAGAAAATGATTAGCTCTTGGAAAG
ACGCAATTAATAAAAAATAAGCGTTCCAGGCAAGCACAGCAGCATCATCAAGATCATGCGC
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTTCACAGCCGG
CCTCCTCCCAGTCAGATGCCATGAAACAAGACAAGTACGTCAGCACTAAACCAAGAAATA
GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA
AAGCACTCTACGACGTTTTGGCCAAGGAAAAGTGAGCATCCACCTCAATCTATTTTGCATA
CTGCAAAGGCCATAGAAAAGTGAAATGAATAAAGTTAACAACCTGTGACACCAACGAAGCCG
CTTACAAAGCCAGGTATCGTATAATTTATCAACAGTCATATCAAAGAATAACCCAGATC
TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCGATGCCA
AGGATCTGGCACCAGCGCCCTTAAAGCAAAAGATAGAAGAAATTGCCAAGCAAAACTTAT
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATTGA
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDFEVPTEKLLRETKVGVENVKFKKSTNVE
ISKLVKKMISSWKDAINKNKRSRQAQQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHKLKRDQVLKALYDVLAKESHPQSILHTAKAIES
EMNKVNNCDTNEAAYKARYRIIYSNVI SKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEEIAKQNLNAQGATIERSVTDRFTCGKCKEKKVSYQLQTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT
GGTCAGATATACTTTTCGCATGGGTCAATACCATGGTCAACCCAACCAGTTCTTCTTTGCG
TTTTCAAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA
GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTTAACTGCAGTCA
TTTTGTTTTCTTGGTCTTTACCTCGAATAGGTTTTCTTGTTTTTGTTATTTGTTTTCTTT
TTGGACCCTTATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG
GGATCTGCCACTGGTAACTTCAAAATAGACAAGACGAAAAAACGGTGAAAATGGGTGATA
GAAATAATACAGAAGTAGATGTTGAATTAGATTAACTGAAGATATATAATTTATTGGAA
AATACATAGAGTTTTTGTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT
CTGATTTTTTCTTACGCCAAGTCTTACCGTAACCGGCTGCCAAAGTGTCAATAACTGGA
GCAATTTCTTCTAGAACGAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC
CACAAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTGCTTGTGGAAGTAT
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATTTCTGTGGTGA
TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT
TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTTSSSDFFFSQLGDESSFDNWNINWSTLTQDLTVTGCSVNNWSSFLRSR
FQVLVSLVFWQCPQFVQVQDWLPMSLLLVEVSHTNLTEITWMVFIHNSVVMLTTGHT
STTGVLVSLTDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG
AATTGAAATCTACGATACTTGATGTTGACATTATAGCACTAGTTCCAGGAAACCCTTTC
GAAAAACACAGCAAAAACAAGAGTACTGTAACCAATGTAACATCTGTACACCAGGGACCC
ACACATTACCAAAATCAAAATTATTTTCTAATGCCTGTTATTTTTCTTCTTCTTCTCT
GGCGCGTGAATAGCCCGCAGAGACGCAACAATTTCTCTCGCAGTTTTTCGCTTGTTTAA
TGCGTATTTTCCAGATAGGTTCAAACCTTTTCATCTGTATCCCGTATATTTAAGATGGCG

TTTGCTTTCTCCGTTGATTTTTTCTTCTTAGTGATTTTTTGCATTAAATCCCAGAAC
AATCATCCAATAATCAAGAATGCCTTCCAGATTCACCTAAGACTAGAAAGCACAGAGGTC
ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT
TTTTTTAGTGTTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT
CAGCTAAGTGTAACAACATATTTCTTTGTGTTTGTATTGCGAACTTTGTATTACCATCT
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGAAA
CTGAGCAAAAAGAAAGTGTGCATAGCCTTTGTCATACTTCTCCTTTATTATACCATGATA
TTCAGAACAGTCATACTGTCTACTCATTTTACGGCTATAAAAGGTAACTTTCATTTAGAT
TATGGAAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG
AGTTACCACGTTTCTTTTGTTCGATAAAATGTCCAGTTGAAAACCTGTTTTACTAACGA
TTTAAAAATTGTATTTTCATTACAATATTTTTTTTGTACAGCCGGTAAAGGTCGTATCGGT
AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT
AACATGGATAAAATACCATCCAGGTTATTTTCGGTAAGGTTGGTATGAGATACATTCCACAAG
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAACCTGGACAAAATTGTGGACATTGATCCCA
GAAGACAAGAGAGACCAATACTTGAAATCTGCTTCTAAGGAACTGCTCCAGTTATTGAC
ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAAGGGTAGAATTCCAAATGTTCCAGTT
ATCGTCAAAGCTAGATTTCGTCTCCAAGTTGGCTGAAGAAAAAATCAGAGCTGCTGGTGGT
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKHRGHVSAGKGRIGKHKRHPGGGRGMAGGQHHHRINMDKYHPGYFGKVGMR
YFHKQQAHFWKPVNLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRIPN
VPVIVKARFVSKLAEEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCTTTTACAATTCCTG
GGAGTTTGGCTATTGCTACCCTTGGTCTTAGCACCACCTTTTTTCCGCTATTGTATTGT
TGAACATAATTTAGTATCTATTTCCATTTCAATTATAATTCACGTTTTTAGCAGCCTCTT
CTTCTAGGTAATTGGAATCTTCTTCTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG
ATCTCAATATGTCCCGATAGGCCAATTTTGCCACCAGATAGTTCGATGGCATTTTATTTT
TAGTCCTTTTGAAAGCAATATCATAAAATATATATAGTTCTCCATGATGTTCCGGGTCAGT
CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTCAATTGCAGAAAATAACGAAAGAAATG
GTGGAATACGATCTGTTATATCTAAACTAAAGCTAACTAACGGAATAAGCAAATACGAAT
CGACCGCTAATTTAACAATATGGTTTTCAGCAATTGGAAGTAGAGTGGCACCAGGAAATTC
CTGGGCTCATTCAACCTGGGAATGTACGCAAGACTTGAAGATGATGGTCTGTAAATTAT
TGAATTTCCCAAAACCTACGAAAACATTCCCTGGTTCCCAGCCTGTGTCTTTTCAGCATT
CTGATGTGGAAGAGAAGCTGCTTGCGCATGATTACTACGTTTGTGAGAAAACAGATGGTC
TGCGGGTGTTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCCAGATTACCCCAAA
AGAAGAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACCTG
TCATACAAACTAACCCTAATGACAAAATACAAGAGTTGCGTTATTTAATGTTCCGATTGTC
TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGCCACCTTG
GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA
CTTTTCCGTTCAAAATTTCCATGAAACATATGGATTTTCAGTTACCAATTAGTAAAAGTTG
CTAAAAGTTTAGATAAACTACCACATCTTCTGATGGTCTGATATTTACTCCTGTGAAGG
CACCTTACACTGCCGGCGGAAAAGATTTCATTGTTATTTAAATGGAAGCCAGAACAAGAAA
ACACCGTGGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCA
AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTCAGCTTATATG
TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTTCGACCAGCCTTTTCGATA
GGAAGGAATTTGAAATATTAGAAAAGACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG
ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT
GCGCAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTCAGGGATGATAAGTTAA
ATGGTAATCATACATCGGTGGTCCAGAAAGTTTGGAGAGTATCAACGATTCAGTTTCAT
TGGAGGACCTCGAGGAAATTGTTGGTGTATTTAAAGGTGCTGGGACGAGAGAAGAGCAA
ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTACAGCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG
AGGATGATGGTCCGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPFIPGLIQPGNVTQDLKMMVCKLLNSPKPTKTFPGSQPVVSFQHSVDVEEKL

LAHDYVCEKTDGLRVLMFIVINPVTGEQGC FMIDRENNYYLVNGFRFPRLPQKKKEELL
ETLQDGTLLDGE LVIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLS DGLIFTPVKAPYTAGG
KDSLLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDRNRYNYNDVKPVFSLYVWQGGAD
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET
GAWEMLRFRDDKLNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG
RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT
CAAAAAGAAAGGTTTGTAAGAGCATTGGGCAGAGAGTATTTGTCTCGGTATAGAGGA
GAAAAAATGTACTGATGCTAATTTGGTGTCTGTTCTTTTATTTTGTAAGACTGT
TTTCCAGAAATGTTTGGGTTTATTTTAAATTTTGAACATTTTTCATCTTTCTC
ATTTTGTCAATTCATTTTCTGTGGAAAATTTCACTGACGCGAAGAAGCGATGAAATTC
CAACATCCTCCCATCATCCCAATATTGGCATAACACACATGCAGCACAGCGAACTGCG
GAGGTCAGAGGCAATGTGGCAGAGACGCTGGCGCGCCTGTATTGTATAATAGTATATTT
ACACTCAATTCATTTTGTATATTAATTAAGTGTGTAAGAAAGCTTCTGAAATCAAGAAG
CCCGTACCAGAAGTTCAATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCCAG
AAGGTGCTACTGTGAGCATCAAGTCCAGAATCGTCAAGGTTGTTGGTCCAAGAGGTACTT
TGACCAAGAATCTGAAGCACATTTGATGTTACCTTCAAGGTCAACAACCAATTTGATCA
AGGTTGCTGTTTCAACAGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCCTCAAGTCTT
TGGTTGACAACATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTTGTTGAAAAGGATGGTGCCAAATTCATTGAAG
TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTACTA
TCGAATTTCCACCAACGTTAAGGACGAAATTTGCTTGTCTGAGGTAACCTGTCTGAAGACG
TTTCCCAACGCTGCTGACTTGCAACAAATCTGTCTGTCAGAAACAAGGATATCCGTA
AATTTTGGACGGTATCTACGTTCTCACAAGGGTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTF TKVMNQLIKVAVHNG
GRKHVAALRTVKSLVDNMITGVTKGYKMYRYVYAHFPINVNIVEKDGAKFIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQICRVNRNKDIRKFLDGIY
VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCTTTCAT
CGATCATTTCCGGATCATCATATCTTCTTGGCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGTCTTCTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAAACCTCGAATACCTTTTGTAAAGCGCTTGTGTTGGTGTACTAACACCGTATAAAACAT
ACTTGGGGTTGATTTTAAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA
CAGAATTAGCTGCCATCAATATCAATTATCAACCCTTATATGACTTTATTGTTTTTGT
TTGTTGGCTAATTAATTGATACAAATCTTTAGGCGAAAAATAAAAAAATATAAAGTAAA
GAAGGAAAAATTAGGCGATATTAACAAATCTAAATAAAGACAAGAAACGAAAAAGAG
GTTAATCAAGTATTGGAATAATGTCCAAAGTGTATTATGCCACAGCAAAATGCAGGTAAAG
CTCATGACGCTGATATTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTTCAG
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTGTAGATAATGAAAATCCAAAGATA
AGTCATATTTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTCTGATGTCTTGCAAGCTA
TTGAGAGAGATGCATTTGAATTATGCCCTTGTGCTACCACTTCATTTTCTGGCGATTTAC
TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAGTTATATTGAGAAATTGGATC
TTCTAGACTCAGACATGAAAAGCATTCCTTTTGGGCATTAAATGGGGTGCCTCAAATG
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA
AGTTTCAACCGTTTGAGATGAGTCAAAATCTTTAACTAAATTTGGAGCCCCACGTTAG
AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
TCTCTGAACGAGGACTAATTGCCACAGGTTTAAATAATGGAACAGTACAAATTTTCAGAAC
TATCTACATTACGCCCCGTTGTACAATTTTGAATCTCAGCATTCTATGATTAATAATTGGA
ATTCCATCAGATCGGTGAAATTTCTCCTCAAGGATCCTTATTAGCCATTGCTCAGGATT
CAAATTCATTTGGTTGCATCACTCTATATGAACTGAATTTGGTGAAAGAATAGGCTCCT
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTTCTAGCTGGG
TCATGAGTCTATCGTTTAAATGATTCTGGTGAACATTATGCAGTGCCGGATGGGATGGTA
AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

ATGATATTGAAATTGAAGAGGATATCTTAGCTGTTGATGAACATGGAGATTCTTTAGCTG
AACCTGGTGTCTTTGACGTGAAGTTTTTGA AAAAAGGTTGGAGATCTGGTATGGGAGCTG
ATTTAAATGAAAGTTTATGCTGTGTTTGT TTAGATAGAAGCATCAGGTGGTTTAGAGAAG
CTGGCGGTAAATAA

YGL213C, 397 aa (SEQ ID NO 106)

MSKVFIATANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLLDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVIFEKLDLLSDMK
KHSFWALKW GASNDRLLSHRLVATDVKGTTYIWKFHPPFADESNSLTNWSPTLELQGTVE
SPMTPSQFATSVDISERGLIATGFNNGTVQI SELSTLRPLYNFESQHS MINNSNSIRS VK
FSPQGSLLAIAHDSNSFGCITLYETEFGERIGSLSVPTHSSQASLGEFAHSSWVMSLSFN
DSGETLCSAGWDGKLRFDVVKERITTLNMHCDDIEIEDILAVDEHGDSLAE PGVFDV
KFLKKGWRSGMGADL NESLCCVCLDRSIRWFR EAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107)

CTGGTTCCAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA
TGGAGGGACAATAGCGGGGGCCTTTGATGGTTCGTGTCCTGAATATGAATGGATTGATGCA
AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAGCAATCCAGTT
GCTTCGTGGGTTGCACTGACACGGTTTCATTAGAAACTCATAGGGACAGGCAACGCAT
CTCCCTTCTGGACCTCCAGAGCGCTGAAATCAATGGATTCTTTGGCCAGCCTAGCCGGAG
TGCCTGTTTTCAACGCGCTTAAGTGAAGCCACCTCATTTTGTAGAGTATTGCTGATCC
CATATGTTGGCTGCTCGCCAATTCTTCTGCTGCAATACGCTTGTCGCCGATGTGAATTT
CTGCACTGAGAAACGTACCTGTAGTGATTATGACCTGATCTGCCCCAACCTGGGTACCGT
CATCCAGAACACACCTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT
CAGCAACTTTGTTCTGCAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTCGGAAAGTTCCC
TTTGCAATGTATTTCTTATATAACTCTCTGTCTATCTGGGCTCTGGGCCCCCACACAGCAG
GACCTTGTCTTCTGTTTCAAGATTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCA
TCAGCCCATCGAGAGCGTCGATTTCTTTTACAAGGATGCCCTTACCCACTCCACCAATAG
AGGGGTTGCACGAACACTTACCAATATCTGTTAACGATGGTGTAAATGAGAGTAGTATGCG
CACCAGTCC TAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCGATGACCA
CGACCTGTGTCTTGGTTGTGGGTGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC
TGAGGACCTGTAAGGGAAATGAAGTACACGAAGACGCCAAGTTGTTACACGCAGCATCG
TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108)

MTLWPHPGSYKIKSATLFC SRDKLGCAFLSESSL CMYFLYNSLSIWALGPHTAGPLLLFS
ILNCTPARSVTLPI SPSRASISFTRMPLTPPIEGLHEHLPI SVNDGVMRVV CAPVLDDA
AAASQPAC PAPMTTTCVLVVGWKL VKEDMVNRLRLRTCKGNEVHEDAKVVTRSI VLWGV

YGL260W, 731 bp, CDS: 501-731 (SEQ ID NO 109)

TACCATGGAACACCGGTGATCATTCTGGTCACTTGGTCTGGGGCAATACCAGTCAACATG
GTGGTGAAGTCACCGTAGTTGAAAACGGCTTCAGCAACTTCAACTGGGTAGGTTTCCGTT
GGGTGGGCGGCTTGGAACATGTAGTATTGAGCCAAGTGAGCTCTGATATCAGAGACGTAG
ACACCTAATTCAACCAAATTGACTCTTTCGTCAGACTGAGCTAGAGTGGTGGTTGCGGAA
GCAGTAGCAGCGATGGCAGCGACACCAGCGCGATTGAAGTTAATTTGACCATTGTATTT
GTTTTGTTTTTTAGTGCTGGTATAAGCTTAACAGGAAAGAAAGAAATAAAGATATATTCT
CAAAAGCATA CAGTTGAAGCAGCTCTATTTATACCCGTTCTCTATCAGTCATCACTACT
TAAACGATTTCGTTAACAGATGCTCATTTAGCACCTCACATATCCTCCATATCTCATCTTT
CACACAATCTCATTATCACTATGGAGATGCTCTTGTCTTCTGAACGAATCATACATCTTTC
ATAGACTTCGTATGTGGAGTATTGTATTATGGCACTCATGTGTATTTCGTATGCGCAGAAT
GTGGGAATGCCAATTATAGGGTGCCGAGGTGCCTTATAAAACCCTTTTCTGTGCCTGTGA
CATTTCTTTTTTCGGTCAAAAAGAATATCCGAATTTTAGATTTGGACCCTCGTACAGAAG
CTTATTGTAA

YGL260W, 76 aa (SEQ ID NO 110)

MEMLLFLNESYIFHRLRMWSIVLWHSCVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK
KNIRILDLP RTEAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTT

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTTCCT
GTGTAGCCTAATGTTTAATGCCTAATTTTTTCTAAAATGCAGCAACATACATATGTTGA
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACA
TTTTAAACATCCGTACAACGAGAACCCATACATTACTTTTTTTAATATCTTTTTGT
CACCGCCTTCTTTTTATTTTTATCCGAAGATCTTTTGAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAATTGAAACTTGGACATAAATCATCATTAAGAAGTATACTGTTAAGA
GAGGCATTCATTTCTGTGTATTATAACGTTTAGCATCAGTTACCCTTGAAAGCCCAACATA
TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTTGAAGA
TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT
CCAAGGTTTTAGAACAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCCGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCCTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCCAACA
CAACTAAGGAAGACACCGTCTCTGGTTCAAGCAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)

MSTKAQNPMDLKI EKLVLNLSVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)

AGCCATGTCGGTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT
CCTTTTTTTTTTGCCATTCTTATACATTTTCTTCTTCTGAAATTAACGTGACACCCA
TACCCTATATACACCCATACCCCTATTTTAAATATAAAAAAGTAACTTCATTTTGAAAGA
CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCT
TTCAGAAGGTCTGCTCTTGTGGCTGGTTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG
AAAGGCCCCCTTCATCTCTGCCGATTGCTGACGGAAAGCAGTAGCGGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCCGTAATATCACAATGTTTCGACTAACGGTTACAGTACGTTA
AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG
ACAACAGGAAATAAACAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACCTGCTAGAA
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAATTAATAAAAACTATC
AACCCCTATTTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA
TTTATCAAGTAACATATCCTGGCGCAAATCAGTTTGGAGAGGCTTAAATGACACGTCAC
AGTGATAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT
GTGGAATAAACCCTTTTCTTCCCAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA
CAACGGAATCATTTTTTTACTAACAGTTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA
CAACTACAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCCGGTGGTTCTTC
TCATGCCAAGGGTATCGTCTTGGAAAAATGGGTATCGAATCCAAGCAACCTAACTCTGC
TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCACTGCTTTCGT
TCCAAACGATGGTTGTTTGAACTTTGTGCGACGAAATGATGAAGTCTTGCTAGCAGGTTT
CGGTAGAAAGGGTAAAGCTAAGGGTGATATTCAGGTGTTAGATTCAAGGTCGTTAAGGT
CTCTGGTGTCTCCTTGTGGCTTTGTGGAAAGAAAGAAGGAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114)

MKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFAKSSPFGGSSHAKGIVLEKLGIE
SKQPNSAIRKCVRVQLIKNGKKVTAFPNDGCLNFVDENDEVLLAGFGRKGAKAGDIPGV
RFKVVKVSGVSLALLWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)

GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
GTATGCTACTGTGCATCGTCATGTAGCACTATTTTACGCCGATTTTTCTTTTTTCTTTTCG
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTTTCTAGAAAGTTCGGAAATGCG
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTTCTTGTTCGGCGATATTCGAACCA
GGTCGGGTTGGGCTAACAGCCGCCAGGATGGAAGAATTAAGAATTTTCATAGAAGCCTTC
AGTTCCTTGGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA
AGCATTAGAACAATCTTTTCTCATTGACAGGTATTCTCATTGCTCTATATATATTTTCTT

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA
GACCCCATTAACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC
TGCCATCTTTTAGTCAGCCCCCTACATTTCGCGTTATTTTGATTGCAGTTCTCCAGTGAGCT
ATTATCCAGAATGTAAAAGGAGGAAAGCAATAAAAGCTAACCTAAGAGCTCCAAAAAAA
GCGATGCAAAATTGTTTCAGAACCTTTGAGGTATGCATTGCTGAAACACCAAAATGGTTATA
CATTAAGCTTGTCTAAGCGGATTCCATATGAACTTTTTTCAAAGTACGTTAATGAGAAAT
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTTTG
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA
AAGATCTGGATTTTAGAGCCATAGGAAAGAAAATTGCTAAGGATCTTTTCCAAGACTACG
AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT
TTAAGGAATCTCTCTAGACCAAGTGTTTGAAGATGTTTTTGTATTGGCTGTGGAGTTG
AAAACATAGATGATGGCTCGAGAGAAAAATATGCACTTTTAAAGATTGGTTTAGTTAAGC
ATGAGGAAGAAAATTCCGAAGGTGGCATCAACGAACCAAGATGCCAATAATTGAATCCA
AAATAGACGAGTCTCACGATGATGTTAACATGTCCTGAATCTTTGAAGGAGGAAGAAGCGG
AGAAAGCGAAAGAACCCTAACCAGGAAGACCAATAAAAAAATGGATAGAGGAAGAAA
GATTGATGCAGGAGGAAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG
AAAGGCAAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAATA
AGCAAAAAACCAAGAGGTCCAGCAAAAAAATTGCAAAATTCCAAATCATTCGCTATCT
CTGAGATTGAGGCCAGCAATAAAAAATAATAATAGCAATTCTGGTTCAGCAGAAAGTGATA
ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTTCTCTGTGTCTGGTAATACAC
TAAAAAAACACGCTTCACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA
ACGAGTCCCTAAGCAGATCTCCCAAGGGAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)

MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKS DANCSE
PLRYALAEATPNGYTSLSKRIPYELFSKYVNEKLGELKENHYRPTYHVVDFFGNQYYVE
DEADEDALLRSALKDLDFRAIGKKIAKDLFDYIELNHRGDELSILSKKDKIFKEFSLD
QVFEDVFIGCGVENIDDGSRKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESH
DVNMSESLKEEEAEKAKEPLTKEDQIKKWIIEERLMQEESESRKSEQEKAKEDEERQKKEK
EARLKARKESLINKQKTKRSQOKKLQNSKSLPISEIEASNKNNSNSGSAESDNESINS
SDTTLDVSVSGNTLKKHASPLLEDVEDEVDYRNESLSRSPKGNIIIEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)

CAAAAAAGTTTTCGGATGAACCGGATTAATACAAGTAAAATCAGCAAAGATATAGAAGAC
AAAATAAGCGTGAAAACAATCATAAACCCTCACAACGGGGTTTTTCAGCTGTTACTCCT
CCATACATACATTTTGATAAAGATATAATGTTATATTTCTTTTCGTAATTTTGTTTTACT
TCGGTTTGCTCTATAGATTTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGTACCCCT
TAAAAGGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTGGATGA
AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT
CTTCTTCATATAAATTGAACATGCCAAATCTCTTTCACATTATCCAGGATAGTTTGGAATG
TGTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA
TTCAAAACAAAGTTTACTGAAATGAAGTTAGATTGAGGAATATACTCAGAGGCACAAAGAG
TTGTGAGAACTCCAAAGTTTAGATATATTTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC
CGACCGCATACATGAGGAGAGGCTATACGGTTCCTGCACATAGCTTAGACAACATCAACG
GCGTAGACACAACCTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG
GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCTCTTCA
ATCATGTAAGGGAATTTGTACTTGGTTCCTGCATTTATGTTCTTTGCATTTTGTTCG
CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAUVPTAYMRRGYTVPAHSLDNINGVDTTKA
SVMGTEQRAAMTKGKSLQEMMDDEVTYLMFLFNHVREFVLGSLHLCSLHFVFAFNHSTT
NGEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTGCTGCACGAACATTAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAAATCCACAACATTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTGTAAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCAGTTTCTCTCTGAAATTTAA

TGTC TTCATCCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTTATTCCTTTTT
AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTTCAAGAGTACG
TAATGGAAAAAGATAAAAAATAAGGACCGTCATAAAAAGAGACGTGATTAAACCTAAAAAT
CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAATTCAGAGTTTTGATTGTTCTTCCTT
ATACACCGCCTAGTGCTACTTTGCAGAGGATTATAGGGCAAACCTATTCGGTTCTTAAGAG
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAAACCTCATTCCAGTTGG
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCTTTTTGGGCTATGGAATGA
TCAACAGCGGAATCAACATCATATTCAACAATATTCATTTTCGTCGAGAGTAATTTGCAAT
GGAAAGTGGTTTTATTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG
AAGGTCCCAAAGATGCTAACAAATTTTCATGTACCGCATTGGGCGGAACGTTTCGACCACA
TTCACGATGGACATAAAATATTGTTGAGCGTCTCTACATTCATCACGTCACAAAGGTTAA
TTTGTGGAATTACGTGCGATTGAGCTCTTGCAAAACAAGAAATACAAAGAGTTGATTGAAC
CTTATGATACACGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAACCGGATCTCT
CCGTAGAACTAGTTCCTTAAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG
AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA
TTGAAAAAGGCATGAGCCATTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG
AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCCTCTG
CTTCGCCAACGTGCACTCCACAAAACCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSOLDIVIVPEFKTSFQLDLSALGKM
YSITRDVLLGYGMINSGINIIFNNIHVESNLQWKVLLPQESTFETWKLELGQGYHSI
EHYALHDNIMEEIEGPKDANKFHV TALGGTFDHIHDGHKILLSVSTFITSQRLICGITCD
ELLQNKKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPEIECLVVS
ETVSGAETVNKTRIEKGMSPLAVHVNVNLGGREEDGWSEKLSSTEIRLLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
CCACGATTGACGAACAAGTTGGTTTGTATCGTTGACAGTTTGAATGACGAAGAGTTAGTGT
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAATCTG
CAAAGACTATTGTGATTTCTGGCAAACCTACCATCCAGCTTGTGTCTCTACTTTCGTGTGAA
TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATTATAGAGAACGTTCT
CTTTTATTTCTATAATGAATAGGTTTCGGGTAACGGTTCCCTTTTATAGGTATTTCTAGAAG
ATGAGAGAAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAGATC
AAAGGTGTCTTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAGTGAAAAC
AAAACCTGAAAGGATAGATCAATGTCTTACAGAGGACCTATTGGAAATTTTGCGCGGTATGC
CAATGTTCATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCTTTTGAAGTTTGCCTCCAGAA
TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATTGAAGCCTTACATTCCAAGTTTGT
CAAGATTTTTCTATTGTGGCCACCTTTTATGAAGATTCTGTTTAGGATCTTATCACAATGGT
CAGATCAAATTTTTTATCTGAATAAGTGAAGCATTACCCATACTTCTTTGTCTGTTGTGT
TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTAGTTTTAAGAAAGC
AAACCAATTATGCCACCGGTGTGTTATGTGCTTGCGTTATTTCTCAAGCATTAGTTTATG
GGTTGTTTACGGGTTTCATCATTTGTCTTAAGAACTTTAGTGTATTGGTGGGTTGTTAA
TTGCATTACGCGATTCAATTGTTCAAACAAGACAACATTCCGTATGCTTCCTGAATTAA
ACAGCAAAAACGACAAAGCGAAGGGTTACCTGTTGTTTGCTGGTAGAATTTTAATTGTTT
TAATGTTTATCGCTTTTCACTTTTCAGTAAATCATGGTTTACTGTTGTTTGGACATTATCG
GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA
TACTAACTTTTTACAATATCACGCTAAACAATACTGGTTTTATAACAATACTAAGAGAG
ATTTCTTGAAGTATGAGTTTTACCAGAACTTAAGCATCATTGGTGGGCTTCTATTAGTTA
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFASRIEGLTDN
AVVYKLPYIPSLSRFFIVATFYEDSFRLSQWSDQIFYLNKWKHYPYFFVFLVVT
SMLIGASLLVLRKQTNATGVLCAVISQALVYGLFTGSSFVLRNFVIGGLLIAFS
VQNKTTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNITLNNYWFYNNTKRDFLKYEFYQNLISIGLLLVNTGAGE

LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123)

CATTTAGTTCTGATTACAGCAGAAATCGTAGCGGATGAGACATTTTCATCAAATGGCCTT
TTTTTTTTTGGGCAATTTTTTATATCTTGAAATGATAGTTGCCTTGACTTTCAACCGTT
CATTTTCATTAAGAAGCTTGACTAAATATGAACATTTCTTAAAAAAAAGGTTGACATATAAA
AATAATCGAATATAAACGATGGAATTTTTATAAAATTAAACACATATATATATATATT
AACTATAAATATGTCAAAGAAACCATACAATCATAGATTTATAACTATCTTTTGGATGAC
ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT
CTTTTTTTTTTCTCGATGAAATTTTGCAAAGAGTTTCGAAATTTTTATTTCAGAGCTGGT
AGAGAAAATTCATAAGGTTTTCTTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC
ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCCTAACCTCAGACATCACTGTTG
AAGTCAACAGTTCCGCTACCAAAACCCCATTCGTCCTGTCGTCGCGTCGAACCGGTTGGTA
AGTTCCTTTTTGCAACATGCTCAAAGAAGCTTTGAGAAAACACACCTGGTCTGAATTTGAAA
GAATTGAAGCTGAAAAGAAGCTCAAAGCGTTGATGAATCCAATGTCGACCCAGATGAGT
TGTTATTCGACACTGAATTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA
AACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA
GTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG
CTGCTGGTGGTAGTTTGGACCAAGATGGCTTTTTCAAGATTATTCAAAAGGCCTTTGAAA
CTTTGACTGATTCACAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTTCGGCATGTTT
CTCTCCAAAGAAGGTTACCGATTATGACTTTTATGAAGCTTGGGGCCCCGTTTTCGAAG
CTGAAGCTCGTTTTTTCTAAGAAGACTCCTATTCTCTCTAGGTAACAAAGATTCTTTCCA
AGAAGGAAGTTGAACAATTCATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCCTTTG
AGTTCCTTGGACGAAGATGTCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG
AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGAAGACTGCTGATAACGCTAGATTGGTCA
AACTTGTTGAAAGAGCTGTCAGTGAAGATCCCCGTATCAAAATGTTCAAAGAAGAAGAGA
AGAAGGAAAAGGAAAGAAGAAAATGGGAAAGAGAAGCCGGTGCCAGAGCTGAAGCTGAAG
CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAATCTGAAGCCAAGGCTAACG
CCTCCGCAAAAAGCTGACAAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCAAGAAAAAGA
ACAAGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG
CCACCACGATTGACGAACAAGTTGGTTTGTATCGTTGACAGTTTGAATGACGAAGAGTTAG
TGTCCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAAT
CTGCAAAGACTATTGTCTGATTCTGGCAAACCTACCATCCAGCTTGTTGTCTTACTTCGTGT
GA

YGR285C, 433 aa (SEQ ID NO 124)

MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLNRNHTWSEFERIEAEKN
VKTVDENVDPELLFDTELADEDLTHDARDWKTADLYAAMGLSKLRFRATESQIIKAH
RKQVVKYHPDKQSAAGGSLDQDGFVKIIQKAFETLTDNKRQYDSCDFVADVPPPKKGT
DYDFYEAWGPVFEAEARFSKKTPIPSLGNKDDSSKKEVEQFYAFWHRFDSWRTFEFLDEDV
PDDSSNRDHKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR
KWEREAGARAEAEAKAEAEAKAEAESEAKANASAKADKKKAKEAAKAAKKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDDELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSLLSYFV

YHR010W, 1472 bp, exon1: 501-531, intron1: 532-1092, exon2:
1093-1472 (SEQ ID NO 125)

GACTCGGACGGAACCGTCTCATATTATACGTTTCACTGAATATTTTTTCACGGAAGAATGGA
AAGGGCCTCGAAAGACGTTAATGCATCCGTACACCTACATCTTTACATTTTTTGTGTTG
CACCTACACTGTTTTTTTTTTTTTTCACCTTATGAGTCCGTGATTTCTTGAAAGAGCCGAT
AACAATATTCCAGGTGGAGTCCCGAGGCAGAATCAAGGCTGCGGAGAGAAGTTCTCTCA
AACTAATGGGAGTGATCCGCTCAGTTCCTCCATCACGACAGAAGTGTCTGAGACAAAGTC
TTTCCAGCAGAGTCCGCTACGCTCTTGCTGCAGAGATTCGCCCGAAGGCAGGTTTCCTG
AAATTCTTTTTCACTAGTAAAGTGTTCGTTTCATGTAAACATACTGCCGTAGTTTTGAGCT
AAAATTAAAGATATATTAGATTTTTAGAAATTTCTTAGATAGTCTCAACGTGTTAAACAA
AAGCATAACCAAGAAAAAATGGCTAAGTTCTTGAAAGCTGGTAAAGTTGGTACGTATC
ATTTTCAGTTTTTGGACATCAACAAAAAACCGTGCAACTGTGGTATTAGAAATCCAAGTT
ATTAGCAGTTGATGTTGTATAATTTGAGTTTGAATTCGAGTATTGTATCTTCATATGGGA
GTAGGGAGGAAAAAGCGTGAGATGTTAGATCTGGGAAAAAACCTTTAAATTTGAATGAT
AGCTTATTAATAGAAATATTGGACAAAAAGATGAATGATTTAGGAGCGAACTAACGATT

ATTCATATTCATTGAGCTATACGAGGCAGTGGAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAAAGCATCAATAGCCACCAAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA
GACCATAGGCACATGTACGCAGGCGACCAGGGCCTTTTATTTACTGTAGTTCTTTCCATG
CCCTATTTAAAAATTCGTGGGCCTATGATAATTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAGAATTCGCCAAACTTTAAGAAGGGTTCACATTTACTAACTATTTCTTTTCCCTTCCT
TTTTTTACACAGCTGTCGTTGTCCGTGGTTCGTTACGCCGGTAAGAAGGTTGTTATCGTTA
AACCACATGATGAAGGTTCCAAGTCTCACCCATTTGGTTCACGCTTTGGTTGCCGATTG
AAAGATACCCATTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA
AGATCAAGCCTTTCATCAAGGTCGTCAACTACAACCATTTATTGCCAACAGATACACTT
TAGATGTTGAAGCTTTCAAATCCGTGTTTCTACTGAAACTTTTGAACAACCTTCCCAAC
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTCGAAGAAAGACACCAAGCTGGTAAGA
ACCAATGGTTCTTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVVIKPHDEGSKSHPFHALVAGIERYPVKVTKKHGAK
KVAKRKTIKPFIKVVNYNHLPLTRYTLDEAFKSVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT
TTAGCCCATACATTTTCACCCATGCACCATTTGGATTATAAAGAAAAAAATTTAATAAAAA
TCTGCCGGGGAAATTTCAGAAGAAAAAAGGAAGGTGTGTTTCGCATTTAACACGGGCCACC
ATAAACTTTTTGTTTGCCACCCATCTAGACGGGATCCGCCCCGCCAAGGCTCTCTTCCTC
TAGCTAGGCAATGTGGCTCTCGGAAAGGAACTCCCACCAGGACGTGGTGGGAAATGCAG
CAATTCCTCTCTGCTTCCCGCTGACCTTTCTTGGGCCAGTTTAGTAAGTATGCTCTCAT
CTTTCATGTGTGCTGTAACCTTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT
AAAAGTTCTATATAGCATTTGCTTTTATTTTAGAGAATACGAAAACACACCAGATAATTAG
TGCATATATATTAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA
AACAGAAGAGAACAATATTTGAGGAATGAATTCGGATGAAATTTCTAGTAGAAGAAAAAAG
CCTAAAATAAAAAAGAAAGAAAGGAAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAATCAACAAATCATGCATTAACCTGGTAACGGAGACTTTAAAG
ACGTGCAAAGAAAGCAATTAATTTTTTAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAATAA
TAGAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGATACTGCTGGGTAATGAT
TTATCCTTCTTTTTTTGGAGCACAAATGCTCACTTTTTCTGTCTCTCTCACTTTCTG
ATGTATCCTACCCAACCCTACAGTTTTCAAACTACTAACATCAATTTTTTTGTGAAACGA
CTTTCGTTTTTCGTTTCTATTTATTTTCAATTACAGGTTTTAGTTCAAGATTTGTTGCACCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC
TACTTCTTGATGTCAAATGCCAGGTTGTTTGAACATCACCCTGTTTTTCTCATGCT
CAAACCTGCTGTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG
GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAASEARKHKLKTLVQGPSYFLDVKCPGCLNITTVFSHAQTAVTCESS
TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTTGCTACATATTATTTTCCATAGCATTTCTCTGTCACAACTTCAAAAATAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAAATAAATCCTGACATTGGAAGAAG
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA
ACAGTGCGTATGTTTCAGACGGAGAGACGACCTCTAGAGAGACGTCCGCTCGGTGCGGCAAC
GCTGACGGTTTAGTTGTTTCGACGGGATGATGGGTTCGCCAGGGGGAGGGAAGGCTTTCC
ACCAAGAGAGGTAATAATTATTCGTCGAAATGAACACTCAGAGATACATCCATATTGTTGACA
ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTTAACGTAAATTGAAGGAGATTAAAG
CAAAAAACAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACCATGTTAT
TTATCTCCATTAGGGCGTGAGAGTGTAATTAGTACACAGGTACTACTAGAATGCTAAAGA
ACTTTTTTAAATATCCTGAATCGTAGGGCAAATCCATGTCAAGCAAGAACTAATAGTTA

TTAAACTTCATTTACTTTTGAGCTAGTTAAATATTTTCATCATTTTCCTAAAGTACTGAAC
ACCTGAATGATACTTTTATTGGCCCTTTTAATAAGAAGCTCTGGTTAGAAAATATATTGAG
GATATCATTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCATACAGAAA
AAAGATACAACATAATTACATGTGCAGTCAAATTACTTTTFTTTAAGATCAATTACTAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCAAAGA
CCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACACAAGGTTACTC
AATACAAAGCTGGTAAGGCTTCCCTTGTTGCTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTTCGGTGGTCAAACCAAGCCTGTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACCTTGAAGA
GATGTAAGCACTTCGAATTGGGTGGTGAAGAAGCAAAAGGGTCAAGCTTTGCAATTCT
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFEKGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTCGTTTTCAATT
TCCATGGTGCACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGT
TGCTCAGCCGCTTCGTGGATATTCTCTTGGTACTTTAAACATGGACCTACGTTCCGCTC
TCGAAAAGACCAATATAATAAAAAGTTATAAATFACATTTCCCTTATTAGGTATACGACCT
CGCGCTTCGAAGTAGAGGAGCCCTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTCACCCACGAC
GTATCAAGTTACTTCCCTGGTGCAATGTCCCACTATAAAAAAATTCCCTGACGCTAGATC
GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTCGTACAA
GGTTACTTCCTAGATGCTATATGTCCCTACGGCCTTGCTAACACCATCCAGCATGCAAT
ACAGTGACATATATACACACACCCACACCCACACCCACACCCACACCCACACACACCCCA
CACACACACACCCACACACACCCACACCCACACCCACACCCACACACACCCACACCCCA
CACACACACACCCACACCCACACCCACACCCACACCCACACCCACACACACCCATCTA
ACCTGTCTCTTAACCTACCCCTCACATTACCCCTACCTCCCCACTCGTTACCCTGCCCACT
CAACCATACCCTCCCAACCACCATCCATCTCTCTACTTACTACTACCATCCACCGCCCA
TCATAACCGTTACCCTCCAATTACCCATATCCAATCCACTACCATTACCCTGCTATTAC
CCTACCATCCACCATGTCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT
AA

YHR217C, 153 aa (SEQ ID NO 132)

MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPTPTHHPHTPTPTPHPHPHTPHPHTTPTP
TPHHTHTPHTTSLNLSLNLPSHYPTSPLVTLPHSTIPLPTTIHLSTYYYHPPPIITVTLQ
LPISNSTITLTPYHPPCPHCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)

TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACCGGAAGACTAA
CGTGCAAGCCAACAGTTATAGAAAAGTACCGTGAGAGAGAAAAAAGATATAGCA
TTCAATGAGGCTTTATTGAGGGGCACGATGCTCTTTTTTTCTTCTGTACTTTATAAATAA
TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG
AGCCTTTTCCAAATCAAGGCTCAGGAAGTGAAGTCTGCTCCTTAGAAGAACAAGGTTTGGATT
TGGTAGGGTTCTTGACGAAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC
TAGTTTATTCGGGTAACAAGTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA
CTATGTAGTAAGTTACACAAAGCAACAAGGATATTATATATGTGACAGAGAAGAATTG
CTGTAGAGATTTCATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT
CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAGAAATTTCTA
AACAAGAAACATCCGAAGAGGAAGATACTGCCGGCAAGCATGAACAAAGGGAAACACTGT
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA
GCGTTTCATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCAT
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCGGGACGATGTTT
CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTCGTCATCATCATCAT
CACCCAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTCGAGAGACCAATTC
GAGCGATGTTGAAAGAACC AAAAAGGAAAAC TGTGATGATTTTCATAGAAGAAGAGGGTT
TGGGAGCTGTTGAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATAACAACAGAAC
CAGAAAATGTGGAAGAAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

GAAGCGATGATCCACGGCACCCAACCTACCAATAAACTTGGTCGTCGCAAACTGGTTA
GAGGTGACCAACTTGATGCAACAACAGTTCCATGTTTAATAACGAATCAGATTCTGAAT
TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGTT
CTTCACCTGTGAAAGAGACAAACAACCTTTCAAATATGAATTCTTCACCAGCACAAA
ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
TTTCCAAGCGCCCCAAACAGAAGAAGGCATATATAGGGATTCTGGTGGTAGAACAAGAC
TACAGATTGCCGTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGCATGAAGCGGCGTTGC
AAGGTCATATTGAGATTGTGGAACCTGTTGATAGAAAATGGTGCAGATGTAAATATCAAGT
CTATTGAAATGTTCCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG
TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACCTATACGTAACGCTAAAGGGTTAA
CTGCGTTTGAATCTGTGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAAGATTT
TGCGTGAAATAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA
TTCATAATGACAAATCTAAAAATGGCAATAATGCTCACACAATAGATCAGCCACCTTTTG
ATAATACCACAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA
TTGATGAGAAAGCTCCGGAAGAGGAATTCTATTGGACAGATGTTACTTCTAGAGCGGGAA
AAGAAAAACTGTTTAAAGCTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG
ATATTACAAGTATCTTTTGGCATTCCGGATTTCCCGTAAATCAAACCTCAAGGGATAATA
AAGATCCCGCTTAAATGGTAGCTGTAGGTCGTGGCCATCTTGGAACTGTTAAACTGCTAT
TAGAGCGCAGGTGCAGATCCAACCAAAAGAGATAAATAAGGGTCGTACCGCTTTGTACTATG
CCAAAAACAGCATAATGGGAATAACAAACAGTGAAGAAATTCATTTGATTGAAAATGCTA
TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATA
ATAATAATGAAACATATAAACATGAAAAAAGAGAGAGAAAAACGCAATCACCCATATTAG
CAAGCCGAAGAAGTGCCACTCCTAGAATTGAAGACGAAGAGGACGATACGAGGATGCTCA
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACCTTCGGATT
CGCGCAAGAGATTGGATGACAATGAAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA
AACGTAAAAACAAATGCCTTGCAAGATGAAGAAAAAATTA AAAAAGTATCTCACCCTCTCTA
TGGAACCTCATTCTCCAAAGAAGGCAAAATCTGTAGAGATAAGTAAAAATACATGAAGAAA
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAAGAAAAGATTAG
AAAAGAAAAGAAAAAAGAACAGGAACCTACTACAAAAGCTGGCCGAAGATGAGAAAAAAA
GGATCGAAGAACAGGAGAAGCAGAAAGTCTTAGAAAATGGAAAGATTGGAAAAAGCTACTT
TAGAGAAAGCAAGAAAAATGGAAAGGGAAAAAGAAAATGGAAGAAATCTCTTATAGAAGGG
CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTCAACGATAAACTTGATT
ACAAAAGATTTTTCGCGCTATATTATTTGTAGACGAAAAAACGATAAATTTGTGCTCG
ACTTGCAAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCAA
CTTCTGAGAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT
TCATTTTCCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAATAAAAGAT
ATGTTGTAAACTTTGATGGGGTTGATTGGACACAAAGATTGGGTATGAGCTTTTGGAGT
ACAAAAAATTTGTTAGTTTGCCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA
ACCACGCAAAAAGAAAAGAAATGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
CACGATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAACAGCGTTCTC
TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCCTCCGTCC
TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEDTAGKHEQRETLSEEVS
DKFPENVASFRSQTTSVHQATQNNLNAKESSEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSPNVRNVDIQNHQPF SRDQLRAMLKEPKRKTVDDFIEEGLGAVEEE
DLSDDEVLEKNTTEPENVEKDIEYSDSKDITDDVGSDDPTAPNSPIKLGRRKLVRGDQLDA
TTSSMFNNESDSELSIDDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQNPKRGSV
SRSNSNKS SHIAVSKRPKQKGIYRDSGGRTRLQIACDKGKYDVVKMIEEGGYDINDQ
DNAGNTALHEAALQGHIEIVELLIENGADVNKSIEMFGDTPLIDASANGHL DVVKYLLK
NGADPTIRNAKGLTAFESVDDESEFDDEEDQKILREIKKRLSIAKKWTNRAGIHNDKSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGHL PYVGTYVENGKIDLR SFVESVKGHEDITSIFLAFGFPVNQTSRDNKT SALMV
AVGRGHLGTVKLLLEAGADPTKRDKKGRYALYAKNSIMGITNSEEIQLIENAINNYLKK
HSEDNND DDDDDNNN EYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDRDVKESTTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSI SPLSMEPHSPK
KAKSVEISKIHEETAEREARLKEEEYRKRRLKLEKKRKEQELLQKLAEDEKKRIEEQEK

QKVMERLEKATLEKARKMEREKEMEEISYRRAVRDLYPLGLKIINFNDKLDYKRFLPL
YYFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDPShLTPLWNMLKFIIFYGG
SYDDKKNNMENKRYVVNFDDGVDLDTKIGYELLEYKFKVSLPMAWIKWDNVVIENHAKRKE
IEGNMIQISINEFARWRNDKLNKAQQPTRKQSLKIPREL PVKFQHRMSISSVLQOTSKE
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAACCTGACTGAACCAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC
GCCCTGAGAGATTTTATTTTCTTATAAATTTTACTAAATAAGGATTTGTACTTTTGATAG
AGTTTTTTTTTTTTCTGACGTTTGTTTAGTTAATATTATATAATAGTATTTAGGAACTA
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTCAATTGTTT
GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA
AAATTGTGTTTTGACATCGGCGTTTAGGCTTGTTTGTCTGTGCACACATACGCTGCTTAC
ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAACCTTCAATAACGATTTTGCGT
GAAGGTTTAATTTTCAATTATTGCAATTTTAGCAGAGAAACGCACATAAATATATATATAT
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG
AAGACTTCGGTTTTAAGTTTTTAGGTCAAAAACAAATCTACCTTCCTTCAATGAAAAAC
TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG
CCTCTGGTAGTAAGGCGGTGGTCGGCGAATTACAATTACTGAGAGATCATATCACCTCCG
ACTCTACTCCGTTTAAAGTTTCAAGTGGGAGAAATCCAGATGTAATATTTGTGTGTCT
TTCATGGTGATCAGGTTTTGGTTTCAACCAGAAATGCATTATATTCGTTAGACTTTGGAGG
AATTGAGTGAATTTTCAACGGTCACTTCTTTTGAAGAAGCCAGTTTTCCAATTGAAGAAGC
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA
CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTCACAAATTCGCAGT
TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTGCATGGCGAAATGGCGAAATGG
AAAAACAATTTGAGTTCTCTCTACCGTCAGAATTAGAAGAGCTTCCAGTAGAAGAATATT
CCCCTTTGAGTGTTTACCATTCTCTCTCCACAGGATTTTTTGGCGGTTTTCCGTAATGTTA
TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAAATGTACATTATAAAGCACATAG
ACGGCAGCGCCTCATTTCAGAAACTTTTGATATTACACCTCCATTTCGGGCAAAATAGTAA
GGTTCATATATATGTACAAAGTTACCTTGCTGGTTTAAATTGAACCTGATGCAACGTA
ATGTGCTAGCATCATCATGTTCAAGTGAAGTAAGTATATGGGACTCGAAACAAGTTATTG
AACCTTCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA
CAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTCAGGCACTATTCTAGAACCTTGTT
CCGGTTTGATAGCATAGAGCGATTGCGCTCGTTTACATATTGAATAACGAAGGTAGCT
TACAGATAGTCGGGTTGTTTCATGTGGCAGCATCAAAAAGCGCCATTATAGCATAAATC
TGGAATCTTTAGAACATGAGAAATCTCTCTCTCTACATCAGAAAAAATTCCTATTGCTG
GACAGGAGCAGGAAGAAAAAAGAAAAATAATGAATCAAGTAAGGCTTTATCAGAGAATC
CTTTCACATCAGCAAAATACATCAGGCTTCACTTTTCTTAAACACAACAGCCGCTGCCA
ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTGGTGCTCCCTCATTGATCATCCGCAT
TTAAAATTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGATGCGTCCAGTGAACAAG
ACGCAACAGATCTCTGCTTCTGCTAAGCCAGTATTTCGGCAAAACCCGCGTTCCGAGCTATTG
CCAAAGAACCCTCAACATCAGAATATGCCTTTGGCAAGCCATCTTTTGGTGCTCCCTCCT
TTGGCTCTGGAAAGTCATCTGTTGAATCGCTGCCTCCGGATCTGCCTTTGGTAAGCCCT
CTTTTGGTACTCCTTCTTTTGGCTCTGGAAATTCATCTGTTGAGCCGCTGCCTCCGGAT
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCTTTTGGCTCTGGAAATTCATCTGCTG
AGCCGCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA
CTGCATCAAGTAACGAACTAACTCTGGATCCATATTTGGAAAGGCTGCATTTGGTTTCAT
CATCTTTTGCACCCGCAACAATGAACCTTTTCGGATCAAACTTTACTATTTCAAAACCTA
CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA
GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA
ACACCTCTACGAAACCAAGACCAATGCCTTTGATTTTGGGAGTTCTTCTTTGGATCTG
GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACCTTTTAAATTCGGTACTCAGG
CTTCACCTTTCTCTTTCACAGTTAGGAAACAAATCACCATTCAAGTTCTTTCACAAAAGATG
ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG
AACAGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC
AAACATCTTCTACTAGATTACCGGAAACTCCCTCGGATGAAGATGGTGAAGTTGTCGAGG
AGGAAGCGCAAAAATCCCCATAGGCAAGCTAACTGAAACTATAAAAAAAGTGCCAAATA
TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAAATCATGTCAAAGCAAAATCCGAAT
CGCCGTTTTTACGATTTGCAACAAATATTACCAACCAAGCTCTACAACACCTGCTTTTT
CGTTTGGTAACCTCCACAATGAATAAAAGTAATACATCTACGGTTTCACCAATGGAAGAAG

CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT
TTCTACCAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC
CAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAGTGCTTTTG
ATACCACAGCAAACGAAGAAATTCCAAAGTCACAGGACGTGAACAATCATGAAAAAAGCG
AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCAGGATAACAAGTCTAAAGAAA
TGAATGAAACTTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTCCAAGGAG
ATGGAATAGCATTTGAAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA
AGCAATTCGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA
GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA
TATCTGAGTCTTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG
AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAACTTCATTAG
AAGACAATTATGCTGAATCTGGCATAACAGACAGACCTTTCAGAAAGTTCCAAGGAAAATG
AAGTTCAAACGGATGCCATACCCGTGAAACACAACAGTACACAACTGTTAAGAAGGAAG
CAGTCGACAATGGTCTGCAAACTGAGCCTGTTGAAACATGTAATTTTCTGTTCAAACAT
TTGAAGGTGACGAAAATTATTTAGCAGAGCAATGCAAACCAAAGCAATTGAAAGAAATATT
ACACAAGTGCAAAAGTATCAAATATTCCTTTTCGTTTCACAAAATTCTACGTTAAGGTTGA
TTGAGAGTACATTTTCAGACGGTCAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA
ATATGGATACTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT
CTATCAATAATCTGTATACTTGGAGAATACCAGAGGCTGAAATTCTATTAATATTCAGA
ATAATATCAAGTGTGAACAAATGCAAAATACAAATGCTAACATTCAAGACCTGAAGGAAA
AAGTTACAGATTATGTCAGGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA
AAGAGGAGTACTCTGTTTTTAATGCATTTTGTGATGCTTCGAGTGGATACGTTAAAGATC
TCAGCACGCATCAATTTAGAATGCAAAAGACATTACGTCAAAGCTATTCGATGTGTCCG
CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAATTTGTTCACTGTAAAGAATA
AGAGATTGGACGATAATCCATTAGTGGCAAAACTAGCTAAAGAATCTCTTGCACGTGACG
GTTTACTAAAAGAAATCAAATTATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA
AAGGTA AAAAGGCTTCGTCGTTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT
TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTTCTTCA
AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136)

MSSSLKDEVPTETSEDFGFKFLGQKQILPSFNEKLPFASLQNLDISNSKSLFVAASGSKAV
VGELQLLRDHITS DSTPLTFKWEKEIPDIVFVCFHGDQVLVSTRNALYSLDLEELSEFRT
VTSFEKPVFQGLKNVNNLTVILNSVNDLSALDLRTKSTKQLAQNVTSFQVNTNSQLAVLLKD
RSFQSFARNGEMEKQFEFLPSLELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE
VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPYMYKVTL SGLIEPDANVNVLAS
SSEVSIWDSKQVIEPSQDSERAVLP ISEETDKDTPNIGVAVDVVTSGTILEPCSGVDTIE
RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSPTSEKIPIAGQEQUEEK
KKNNESSKALSENPFSTANTSGFTFLKTQPA AANSLSQSSSTFGAPSFSGSAFKIDLPS
VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSFSGSKSS
VESPASGSAFGKPSFGTPSFGSGNSSVEPPASGSAFGKPSFGTPSFGSGNSSAEPASGS
AFGKPSFGTSAGFTASSNETNSGSI FGKAFGSSSFAPANNELFGSNFTISKPTVDSPKE
VDSTSPFPSSGDQSEDESKSDVDSSTPFGTKPNTSTKPKTNAFDFGSSSFSGFSKALE
SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP
NVSGNDLTDSTVEQTSSTRLPETPSDEGEVVEEEAQKSPIGKLTETIKKSANIDMAGLK
NPVFGNHVKAKSESPFSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEADTKETS
EKGPITLKSVENPFLPAKEERTGESSKKDHNDPKDGYVSGSEISVRTSESADFDTTANEE
IPKSQDVNNHEKSETDPKYSQHAVVDHDKSKEMNETSKNNERSGQPNHGVQGDGIALKK
DNEKENFDSNMAIKQFEDHQSEEDASEKDSRQSEVKESEDNMSLNSDRDESISESYDK
LEDINTDELPHGGEAFKAREVSASADFVQTSLEDNYAESGIQTDLSSESKENEVQTDAL
PVKHNSTQTVKKEAVDNLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSKVS
NIPFVSQNSTLRLIESTFQTVAEFTVLMENIRNMDTFFTDQSSIPLVKRTVRSINNLYT
WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYFLFL
MHFDDASSGYVKDLSTHQFRMQKTLRQKLFVSAKINHTEELNLILKLT VKNKRLDDNP
LVAKLAKESLARDGLLKEIKLLREQVSRQLLEEKGKKASSFDASSSITKDMKGFKVVEVG
LAMNTKKQIGDFFKNLNMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:
943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATTCTATAATATCCACTGTTTCATTAAACGAATATTGGTCTT

TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTTCTATTT
TTGTGCTCCGTGTCGATATTTCTGTGGAGCAAAACCAGAAAAGATGCGGAACCTCTTAGCAC
TCCGCCTGGACATAGGCGGAGCATATTCCTCCTATGGGATGGGTTTTGTTGTACTCTTTT
CTCTCTAGACAGGACCTCCGATTGCCCTCCCTGAGGGTGAGATGGTTTTCCGGCCTCAGGAC
GGCCTTCTCCAGTTTTCTAGCGAGGCATACATTCCAACCAAAGGTGTATCAAGAAATATCTG
AAATTAAGGTAGTTGAATCTCTATTTGTTGTTGTTATTACCGCTTATTATCCCATAGTT
GAGACGACCAAGATTCAAACATGCAAATGTATGCACCATATCCATTCTAAACATAGTTTT
TCGAACGTTTCAAGCTTAAAGGGACAATTATTTTAGAAACTGAATTTTTTACCCAGTGGA
TAACATCGTATCTGTAAAGTCTACAAAATTTTTTATCCATCAAAAATTAAAACAAAGAAA
ACTGCCAAACTGAATATGAGGAACCTTTCCTCTCTAGGAATGACTTAGTGAATGTACAGTG
AATTGTGGAAAAATATGATTAGATTTTGAGCGGGTGATGCGACTTAACAGTCTCATTGCCT
AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT
TAAAAATTTTGTCTTCTTCCGAACAGTTTATGAAAAAACTATTACGTGTTTTTTATGATATCC
TTACTAACTTGTCAATTTTTTTTATAAAATTATTTTTTTTAAACAGTTTTGTCAAGACTTTGAC
TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA
GATTCAAGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT
AGTCTTGAGATTGAGAGGTGGTATCATTTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA
CAACTGTGACAAATCTGTTTGCCGTAAGTGTTATGCTAGATTGCCACCAAGAGCTACCAA
CTGTAGAAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAGAAGAAGTTAAATG
A

YIL148W, 128 aa (SEQ ID NO 138)

MQIFVKTLTGKITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRITLSDYN
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDKSVCRCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)

AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA
ACTAACAATAGCACCGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAAT
GATCAAGCTTCCAACGAGTGATGTAATATTAACAATGTAATTATATAAATATGAAACAT
CTACATATTTTAAATGTCACTAATGTCAATTACAGAGGACATAAAGTGATTTATGACACAT
CCGTACTAGTAGTTAAGTATGAACAAATTTTGGGTTTATTTTGCCATTTTTTTTACCGCG
GTTTCTTGGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG
CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCACATTA
AGCACTTGGTTCTGTTGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA
ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAATTTATGG
AACGAAAGAGGCAGGCCTTAGTGGAACGATTAAAAAGAAAGCAAGAATTTAAGAAACCCC
AGGATCCTAATTTGAAGCCATCGAGGTACCTCAATCTCCTACCAAAAACCGTGTGAAAG
TGGGGTCTCATAATGTCTACACAACAAGGCAAAAATTCGAAGTTTCAATATTAATGAAG
TAAGGTTATCTCAATTACAGCAGCAACCAAAACCACAGCTAGTACAACCACATACTTTA
TGGAGAAATTTCAAACGCAAAGAAGAAGCAAGATAAACAATTGCCAAGTTTGAAAGCA
TGATGAATGCAAGAGTACATACGTTCACTACCGATGAGAAGAAATATGTGCCGATAATCA
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG
ACTTAAAACGGGCTTTGCATGAGATCAAATCCTTCGGTTGGGCAAACCTTTTTGCTAAAA
TTCGCCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCTCATTA
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATCTTTCATGTCA
CCATAACGGACTTTCAGCATACTAGATGTTTATATCTTTCGGGAAAAAGGGGTGTAGAAA
GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAACCCAGAAGTACTACCAT
GGAGACCCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT
TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA
AAAAGACTCACAAAAAATGTGGCTCTCCCATTAACATATCTCTTCATAAGTGTTGCGATT
ACCATAGAGAAGTGCAATTTCTGTGAACAAGTGCTAAAAGAATTGAATTAAATGGTGGGT
ACGCTTGGGCGCGCTACGAAAGTGGACTGTAACCAAGCCTATATAAGGCCAAAGGGG
AAAACGGGTTTAAATATAATCAAAGGTACTCGTAAGCGCCTGTCAGAAGAGGAGGAAAGAC
TAAAAAGAGCTCTCACAATTTTACGAATAGTAATCTTGCCAAAGCATTTTTTCGACGAGA
AATTTCAGAATCCAGATATGCTGGCAAACCTTAGACAATAAAGAAGGAAAATAATAGAAA
CTAAGAAATCGACAGCACTGAGCCGCGAACTAGGCCAAAATTATGAGAAGGAGGGAATCCA

GCGGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAATGAAACGAACCACAGAAAGTG
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTTCGATCCCCTCATGGAAAAATTTCCC
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAAAAAAA
AAACTGTTATAAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAACATTTCCGGAT
CCAAGGAAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)

MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSHNATQOGTKFEFSNINEVRLSQLQQPKPPASTTTTFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFNLWVKRYIPEDDLKRALH
EIKILRLGKLFKIRPPKFQPEYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYYNLRLGDVIAILNPEVLPWRPSGRGNFIKSFNLRI SHDFKCILEI
GSSRDLGWCPIVNKKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGGYALGAPT
KVDSSQPSLYKAKGENGFNI IKGTRKRLSEEEERLKKSSHNFNTSNSAKAFFDEKFNPD
LANLDNKRRIIETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGFDPTHGKISQVLKSSVSGSEPKNLLGKKKTVINDDLHYKKEKVILAPSKNEWFKK
RSHREEVWQKHFGSKETKETSDGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)

GACATTTTGAAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG
AAATGACTTACTATGAAAAGACACCTTTGATTCGTCAATTTTGAACAATGGTAAGACAA
ATTCTGTGGTTTTACGTTAAGCATGAGATGTTACAACAGGTGGAAGTTTCAAATCGAGAG
GAATCGGGCATTTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC
TTGCTGTATTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT
CGATGGCACTTAATTGCAGTGTAGTGGTTCCTAAAACTACAAAACCTAGAATGGTAAAGA
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAAACATGGTTCGAAGACATATATG
TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA
TAGAACAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG
TTGGTGGTGGTGGGCTATTTAGTGGCATAATTAAAGGCCTAGATAGGAATCAGCTTGCTG
AAAAAATTCCGGTCGTTGCTGTAGAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA
AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTGCAACTTCTTTGGCCTCCC
CATACATAGCATCATTCCGCTTTGAGAGTTTAAACAAGTATGGATGTAAGTCTGTAGTTT
TATCAGATCAAGAGCTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG
TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA
TTCTGGAACAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCCGGTGGATCAT
GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHGSKTLVHPFDNETIWEHSTIVDEIIEQLKENDISLPRVKALVCSVGGGGGLF
SGIIKGLDRNQLAEKIPVVAVETAGCDVLNLSLKKGSPVTLEKLTSVATSLASPYIASFA
FESFNKYGCKSVVLSQDQDLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACCTCAGCATGTGCTACTCCAGTTAATGACTTGTTTCGTATCGTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT
CAAGAGCGTATAGCCAAACGACGACAGCTGTCTCATATGTTTAAATGCTGCATAGTGT
GAGTCTCTAGTTTTTACCAGCAGCCACCAGCCGCTTCTCGAGCAAAGTGATAGTCCATT
AGGACTCATCATTCATCTAATTTTGCTATGTTAGCTGCAACTTTCTATTTTAAAGAACCC
TTCTGGAAATTTACCCGGCGCGGCACCCGAGGAAGTGGACAGCGTGTGCAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT
CTAAAGATTAAAGTGTTACTGTTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTGGTCTGTACGCCCTTTTTCGTGGTAATATTACCTTTACAGAATTCTTTCC
ACTCCTCCAATGTTTTAGTTAGAGGTGCCGATGATGAGAAAACCTACGGAACCTGTTATCG
GTATTGACTTAGGTACTACTTATTCCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTACCCGATGATG

AAAGATTGATTGGTGTGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT
TCGACATTAAGAGATTGATCGGTTTGAATATAACGACAGATCTGTTTCAGAAGGATATCA
AGCACTTGCCATTTAATGTGGTTAATAAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTC
AAGGAGAAAAGAAGGTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAAGATGA
AACAAATTGCCGAAGATTATTTAGGCACTAAGGTTACCCATGCTGTCGTTACTGTTCCCTG
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA
ACGTTTTGAGAATTGTTAATGAACCAACCGCAGCCCATTGCCCTACGGTTTGGATAAAT
CTGATAAGGAACATCAAATTTATGTTTATGATTTGGGTGGTGGTACTTTCGATGTCTCTC
TATTGTCTATTGAAAACGGTGTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG
GTGGTGAAGATTTTACTATAAGATCGTTTCGTCAATTGATAAAAGCTTTCAAGAAGAAGC
ATGGTATTGATGTGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA
AGGCTAAACGTGCCTTGTCAGCCAAATGTCCACCCGTATTGAAATTGACTCCTTCGTTG
ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAACCTAGATC
TATTCAAGAAGACCTTGAAGCCTGTCGAGAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA
AGGATGTTGATGATATCGTTTTGGTTGGTGGTTCTACTAGAATTCCAAAGGTCCAACAAT
TGTTAGAATCATACTTTGATGGTAAGAAGGCCCTCCAAGGGTATTAACCCAGATGAAGCTG
TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTGCAAGATA
TTGTTTTATTGGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCTATGA
CTCCATTAATTAAGAGAAATACTGCTATTTCCTACAAAGAAATCCCAAATTTTCTCTACTG
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA
AGGACAACAATCTATTAGGTAAGTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG
TACCTCAAATTGAAGTCACATTTGCACCTTGACGCTAATGGTATTCTGAAGGTGCTGCCA
CAGATAAGGGAACCTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT
CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAACCTACGCTCACTCTTTGAAA
ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG
ATGCTGCTAACGATGTTTTAGAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG
ACTTTGATGAAAAGTTTCAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT
ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG
GTGATTATTTTGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSSNVLVRGADDVENYGTIVIGIDLGT
YSCVAVMKNGKTEILANEQGNRITPSYVAFDDERLIGDAAKNQVAANPONTIFDIKRLI
GLKYNDRSVQDKIHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAVVTVPAYFNDAQRQATKDAAGTIAGLNLVLRVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGGTFDVSLLSIENGVEVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLRAKFEELNLDLFKKT
PVEKVLQDSGLEKDVDDIVLVGGSTRIKPVQQLLESYFDGKKASKGINPDEAVAYGA
QAGVLSGEEGVEDIVLLDVNALTGLIETTTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNNLLGKFELTGIPAPRGVPQIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRLTQEEIDRMVEEAKEFASIDASIKAKVESRNKLENYAHSLKNQVNGDL
GEKLEEDKETLLDAANDVLEWLDNDFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCGGTAGTTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTCCCTTGAGACTACTTTGGGGACTTTAAAAAAGTAAAAACAGTAA
CACGTTAATCTTTAGAATTACATAGCCATATTTATATCTTCCAGAGAACCCTTTTCGTGT
CCTTTATATAAAAAAGCAACTTTTTCGACACGCTGTCCAGTTCCTCGGGTGCCGCGCCGG
GTGAAATTTCCAGAAGGTTCTATTAAAATAGAAAGTTGCAGCTAACATAGCAAAATTAGA
TGAATGATGAGTCTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA
AAAACCTAGAGGACTCACACTATGCAGCATATTAACATATGAGGACAGCTGTCCGTTTGG
CTAGTACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATGACGATCAACGAACAGTCATTAACTGGAGTAGCAC
ATGCTGATGTTTATGGGGATCGATCAGATCAAGCGATGTTGGGCTCCCGAGGAGTTGTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCGGTGATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGGAAGGTTGGTGTTCGGTTGTGGCAACGAGAGATTTGGAG

GCAACGGTACTGTCCTTGTCAGTAAATCATGATACGTGTACATTAGTGCCCAAGAACAATA
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA
GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG
TGTTGGATAAAAACACGTTTCCGCCTATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT
TCATTGAGACTTTTGGTGATGATTACAGGACTTGTTTTGCGAATAAAGTTGACTTGTTCCA
GTAATAGCGTCGATTGGGATTTGATTGACTCCCAAGATAATATAATCCAAGAACTGG
AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFVCGNERFNGNGTVLS
VNHDCTTLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTECFANKVDLSSNSVDWDLIDSHQDNIIQEELEEQCKMF
KFNVHKHKS

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
GTTTCATCTGCCCTTCTTGAGCGTGTTTCAGCAACTGGCCTACCAGCGGGACGCCTTTGGGT
AAAGTTACCAGTGTTCGCATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA
GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG
ATATTTAAAGCAATGTACAAATACATACACAAATATCACTGTAAAAAATTGCGAAGAA
ACTTGAATTTGAATATGATTCTGCCACTTTTTCTTGCTGTCATTTATAGTCAGAAATG
AAAAATTGTCCGAGAAATTAAATATAATATATGGAAGGACATTTAGTTTAAAG
AATTTGATTAAATGTCCTCTCAATATCCTCTGTAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG
AATATCAAATTTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTGT
CAGAGAATGACGGTGATGTCTCCCCATCTGTTTGAACAGAAAGGAAATATCAGTCGATG
ATATGGATATGATTTCTTTGCCACGGAATTTGACAGGCAAATGGTTTTAGGTTTACCTA
TGTTTTTCGATCTTGAAGACGAAGAAACAAATATGATCCACTTCCTTCAGTTTCCCATC
ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATGAAAG
CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTTGGTTTCTCAAATGAGAA
AAAGATACATTTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA
AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTTTGGAGATTTGAAGACGATAAACGAT
TCCAAGATCCCCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT
ACACAAATCTGGTTTGAAGGAAAAGGAAATATAAAAGTACCATAACCGGTGAATATT
TCGATTTAGAGGATTACAAAAACAATACATTTTACCATTTAAGTAATCAGGAAATACGC
AAAACCCACTTTTCACTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTAAACAG
ATGTGCCTACGTTTCAAGAATTTAGGGATGATTTTGCATACATAATAGAGTTAATCCAAT
CTCATAAATTCACGAGGTTTACGAAAGCGATTATCTTATTTATTAGATAAATTTGAAT
TGTTTCAGTACCTAAACTCTAAGAAAGAAATTTTAGCTAATAAAAATGTTCCCTACAGAG
ATTTTTATAATTTCTCGTAAGGTAGATCGAGACTTGCTTTAAGTGGTTGTATTTCTCAAC
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCTGAAAGGATAGTTTATC
AAGACCCGGAACGTCAGGAAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT
CTAATGACCAACCCATTGCGATTGGGTGAAATTTGATTGATGATGAATTTTGGATTGGT
ATAGAAATATTTACCTAATAGATTACCATCTAACTCCTAACAAAGTAGCAAAGTTGGTCG
GCAAAGAAATGAGGTTTTACCTATTAGCCAAAGTGTTTCTGGAGTTTGATAATTTTATTG
AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTTCATATCCTCGAAAAATCAA
AGTACCAATTGGCCCAAGTATCAGTTAATTTTCAATTTCTATTTCCAGTGGTGAAGACTGGT
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA
ATATACAAATTTGCGAGATTTTTCCCAACTATTCAAGGAAATGTCGTGTCAAATTTTCC
AGGAGTTTTTGGATCTTATCTTCAATCCTTTATTCACTCTGGAAAAGGAGCAGTTACCAA
TAGATTTCATCTGTAAATACTGATATCATTGGTCTGCAGTTTTTTTTTATCAAATGTGTGTT
CTATGGATCTGGTCATTAAAGAGTCGGATGAATATTACTGGAAAGAATTTACTGATATGA
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAACCTGTTGCGCATTACATGT
ATTATATTTATAAAAGTTTAGCGAAAGTTAATTTTCTGCGGTCACAAAATCTTCAAATA
CAATCACCCCTAAGAAATTTATTGTTCTCCACTAGTCCAGCAGAACTTCCCAATTTGGAGTGG
ATTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG
GTCTGCTACAGGTAGAACCGCTTTGGGATACTGCAACAATGATTCAATATTTATTTATC
TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCATTACTGAATTCGCAA

AATCGACCTTTTTGAAGAATAAAAAACGTGCTTCTAGAACATGATTATTTGAAAGACCAGG
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAAGATCATATGAGA
CAAATCCTTTTCATGAAAATGTTTAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA
TTCTTTACAATAGTTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTATTTACTTGCTGAACCCAACAGATTTGTGCGAGTTGTCGAGAACAGTGTGCTATCTA
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAACGTGGGTGGGATAGATAATTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCACACGTTCCGATGATTAGAGAAGATATAGAAAGGAGACATTGGATCAAGAGT
GGAACCTTCGTTCCGGATCACTTTGGAGTAATTAACCTCCATTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRPSLLFDEYQNSVTKPNETKNKEARVLSSENDGDVSPSVLKQKEISVDDMDMISL
PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYNGESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMRKRYIAASKQDGISNIKNDEKWFLYPKPLPKFWRFEDDKRFQDPDS
DLNDDGDSTGTGAATPHRHGYYPYFYTDHYYYTKSGLKGKGNIKVPYTG EYFDLEDYK
KQYIYHLSNQENTQNPLSPYSSKEESLEEFLTDVPTFQEFRDDFAYIIELIQSHKFNEV
SRKRLSYLLDKFELFQYLNSKKEILANKNVPYRDFYNSRKVDRDLSLSCISQRQLSEYI
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFDLDWYRNIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV
SVNFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSINFQEFDLI
FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW
TAQGDNPPTVAHYMYIYKSLAKVNFRLSRQNLQNTITLRNYCSPSSRTSQFGVDLYFTDQ
VESLVCNLLLNCNGGLLQVEPLWDATMIQYLFYLFQIPIAAPLSSVSLNQSSTFLKN
KNVLEHDYLDKQETAKINPSRDITVGEQRSYETNPFMKMFKMGLKISLSSKSILYNSSY
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGKKAPYFEENVG
GIDNWDYDTAKDTSIKHNVPMIRRRYRKETLDQEWNFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTCGCTTCGTTTACTTTTCTCTGCGTGCTCGAGAACTGATAAAATACTGGTTTAGGA
AAACCGTCCACTTATGGATTAAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT
AGCAACGCTACGCACCTAGCTGTGTGTGCTTGCTCTCTTGTGTTTCGTCTTTCGTATATTGC
GGGTTCCCGCGGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTGCAAGAA
TTCTCTAAACATATTCTATACTTCAAAGTTTCTAGCTTCTTGCTTTTCGGTAGTTGCCA
AACCAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACCTAAAC
AACTTAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCCTAG
TAGCCGTCAAGGCACAAACCACGTTTCCAACCTTCGAGAGCGATGTGCTGAACGAGCATA
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTTCGGGTGTCTTAACGCATTCGGATG
GCCCATATGGTGAGAACCTTGCCCTTGGTTACACAGACACGGGAGCGGTGGACGCCTGGT
ACGGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAATCCACGGGTCACT
TCACACAGGTGGTTTGGAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA
CGACATGGAACAATTATATTGTGTGCTCCTACAACCCTCCTGGAAACTACCTGGGTGAGT
TTGCAGAGGAAGTGGAACCACTTATAAGCACTGTTTCTCCTCGTCCTCATCCTCGTCCTCTT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG
CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAATCGACGA
CCATAAACCCCTGCCAAGACCGCTACCCCTCACTGCGTCCTCTTCTACCGTAATTACTAGTA
GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT
CCTATGCTACCTCCTCGAGTACCGTCTCTAGTGATGCTACTTCACTCAGTACCTACCACCA
CCTCATCGGTTGCTACATCGTCCAGTACCCTCTTCCGACCCTACCTCGAGCAGTCTG
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTTCTTCCAGCGGAGTACCG
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT
TGAGTAGTACTCTTACTACTTCCACCGCAAGCTCCAGAAGTGTAACCTCCAATTCAAGTTA
ATTCTGTTAAGTTTGCAAACACAACCTGTGTTTCTGCTCAAACAACCTCTTCTGTAAGCG
CCTCATTATCATCATCTGTAGCTGCTGACGATATTCAGGGTAGCACTTCCAAGGAGGCCA
CAAGCTCAGTTTCCGAACATACTAGTATAGTAACCTAGTGCAACTAATGCTGCCCAATATG
CAACGAGAGTTGGGTACATCTTCCAGAAGTTCTTCCGGGGCGTCTCTTCTCCTCAGTGTGT
CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA
GTAGCACAGCCCATACCACAAAGGACACCGCCACCCTCAGTAACCGCCTCAGAAAGTA

TCACTTCGGAACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG
CCACATCGAGTAGCATTACTCCAACAGTGCTTCTGTGTCAGGACACGGTGTAACATACG
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA
CAAATTGCTCTAGTATCGTGAAGACCACAACCTTTAGAAAATTCGAGTACCACAACCATCA
CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACCTCCACAAGGGCAG
CTACCGCAGTAACCATAGATCCACATTGGACCCTACCGACAACCTCAGCTAGTCCAAACCG
ACAATGCTAAACACACCTCTACATATGGATTCTTCTTCCACAGGCGCATCTTTAGTACAGCT
TAACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA
CTTCCGAGAGCGATTATTCCGATAGTCTAGCTTCCGCATCTCCACTGCCACCACCCTG
AAAGCAATCTGATCACAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA
CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAACAATCTCGACATCTTGTA
GCACTTTGAACGGCGCCTCAACCCAAACAGTGAGCTAACCACATCGCCTATGAAAACCA
ACACGGTGGTTCCAGCTTCTTCTTTCCCTTCAACTACAACCACTTGTCTAGAAAATGATG
ACACTGCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAACCCCGGAG
AAACACTTCTCTCGCTAGCTTTCCGCACATCTGAAAAGCCAAACGAGCCCACTTCTG
TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACCTACCAACAGACTGTTG
CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACCTACTGGTAGCA
ACGGTCGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACCTTCCTCGA
TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAACTTTCTGCATACGAAGGTG
CTGCAACACCTCTTTCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG
TCGTAGCTGTTCTGTTCCGCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGCLVAVKAQTTFPNFESDVLNEHNKFRALHVDTAPLTWSDTLATYAQNYA
DQYDCSGVLTHSDGPYGENLALGYTDTGAVDAWYGEISKYNYSNPGFSESTGHFTQVWVK
STAEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD
TVSTISSSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSSTESVGS
STVSSASSSSVTTSYATSSSTVSSDATSTTTTSSVATSSSTTSSDPTSSTAAASSSDP
ASSSAAASSSASTENAASSSSSAISSSSSMVSAPLSSTLTSTASSRSVTSNSVNSVKFAN
TTVFSAQTTSSVSASLSSSSVAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS
SRSSSGAVSSSAVSQSVLNSVIAVNTDVSVTSVSSTAHTTKDTATTSVTASESITSETAQ
ASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV
KTTTLENSSTTTITAITKSTTTLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS
TYGSSSTGASLDSLRTTTSISVSSNTTQLVSTCTSESDYSDSPFAISTATTTESNLITN
TITASCTSDSNFPTSAASSDDETAFTRTISTSCSTLNGASTQTSELTTSPMKNTNTVVPAS
SFPSTTTTCLNDDTAFFSSIYTEVNAATIINPGETSSLASDFATSEKPNPTSVKSTNE
GTSSTTTTYQQT VATLYAKPSSTSLGARTTTGSNGRSTTSQQDGSAMHQPTSSIYTQLKE
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCCATTTCTAGAGGAGTTTTTATAGTCCTGCCATCTAAT
GTAGAGCAATCTTTCTTTCTCAACATCCCTATTTAGTGACACCTTTTCCCAAACCTTCT
GTGAAGTTTTGCTCAATCTATTTGTTTCCGTAGGAGTGTTATTCTCAATCGTGTTGTCTG
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCCTTAATGATGGCAGCATTCCGTATTCTCTTTTGTAGGGTTTCG
TTTGCCTTCAAGTGTTTTGTCTTATTTAGCCTTTTCTTTTACCTTAATTTTTTTCTTTT
CTCTGAAGAAAATGAATGAGTTTAAAGATATAGCAATTA AAAAGTAACAGTGAAGAAAT
TCTCAGATGAGCAGATGGGAATTAAAGAACTATCTACAGAGCTCTTACTAAATTGAATC
AATAATACATACTTACAAACATGTACAGATAGCACAAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT
CTTGCGGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCACATG
CCGAAACTGTTCTTCTGGATCAAAGAAAAACATTAAAGATAAAGAAAGAACTATTTAGAAA
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAACGTATTTGGATTTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC
ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT
GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCTGGCGTTTCTTA
AGCTCACTGTCAATTTCTGTGTATCTGTGACATGTTTGTAAGTATGTATTATTGATTCA
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTTCCCATCTGCTCATCTGAGAAATTT
TTCAGTGTACTTTTTAATTGCTATATCTTTAACTCATTCAATTTTCTTCAGAGAAAAGA
AAAAAATTAAGGTAAAGGAAAAGGCTAAATTAAGAACAAAACACTTGAAGGCAACGAAAC
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAACTGCCCCGATTCTACTCATTAAATGCCAGCCACTGGGGACAGACA
ACACGATTGAGAATAACACTCCTACGGAACAAATAGATTGAGCAAACTTCACAGAAGT
TTTGGGAAAAGGTGTCACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG
ATGGCAGGACTATAAAAACTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAAGTCTC
TCTTAGCATACCTATTAAAAACTGGAGTGGTTCGTCCTATCCAGTCTTTCCATCAAACTC
ACTCTTTGCCACTAATTCATTAGTGGCAAGATGCATAGATTACAAATGACAAATGAGC
CTGGCTGTGACCTCAATTAGTTGCAAGATTGGAGGCAACAGTGATGTTATAAAAATC
AGTTGTTAAGATATTTAGATACCGATACTTTATTGGTCTTTTCCCTATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG
AGTTTTTACGCACTTTTCATCCGAGTCTAATATTCGACTACAAATTTTAGATGCCGACA
TCCATGGGTTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAATATA
TGAGCAGCTTATCACCATGGGATCTTGCAATTCTTGAAAAACTGTATTAACCACAAAGT
CCTTCATTTGCGGCGTGCTATTATTAGAAAAATAAAAGATACTGCGAATTAATTTCCCG
CCTTGAAAACTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AAATTCATACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGCIFVNSIRLKLPRFYSLNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVSL
LRDVEKGKIALQLDGRITIKTPLNGIIVDNAKSLLAYLLKLEWSSLSLSIKTHSLPLTS
NVARCIDLQMTNEPGCDPQLVAKIGNSDVIKNQLLRYLDTDLLVFSMNEFEGRLRNA
QNELYIPIIKGMEEFRLNFSSESNIQLQILDADIHGLRGNQQSDIVKNAKKYMSLSLSPW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTDMDNIVRAATLETIFQVEKWGEV
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAAACGGTGCTTCTAAT
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA
AGAGGTACGTGTGCTAGTGAAATAGGTCACATGTACCAGAAAATCAAGAAATCTTAGATG
TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTATTTATATAAACAAAGATATA
ATTTTTAAAAAAAATTAGAAAAAGCAATATAATTCAGGTCCCACTTGAATAATGGCA
CTGTATTGATGCATTTTCTTATGCTTAGTGACGCGTTTTTCGCGCGTCAGTTTCAAGTTT
TTCTTGGCTTTTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAAGGATTAAAAATGCAGTA
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCTTCCAG
GACAGTACGCGCAAACCTATTATGGAGATATTCAAGGAAGAAGAAGAAGCTTTTTTCGG
CGATAGAAGGTATAATATATGCCTGTGAGGTGTATGACCTGTACCCCGTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT
ATACAATACTCAATAACATTTAGATATACAAGCCTATCTTTCTACTTGGCTTAGGGATC
TTGGAACGACAGGTCCATACCAACAATCTTTTCAGAAAGTATTTCTCTCATGTTTGACC
GCACGTATCTATCTTCAGGAAATGTACGATAGAGGGAGGTTTTCCACATTTGATCGCAC
GTTCTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT
TTTTTTCAAGCTACGATTATGCTTTTCGGGGTGCATACAACTTGTAATTGCTCTGAAT
ACAGGTATGACGAAGTTCATTACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA
AGATAGATCCTGCTGAAGTCATTAAAGGGAACATTTTAGGCTTACAATTCGAAATTTA
ACATATCTAATATATTAATTGAAATTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG
TGAACCTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCGCAGTATCT
CCGAAGGTAATCATCAGGTCCTAGAATTGGGGAGAAAGTTAATGTTTCCATTGTTGAGGA
CTGGAGATTTTGAAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG
CGAAGGATGTAAACTAGAAATAACAGTCTGGATGAAGTTTCCCTGGGTAATGCAGTGGGA
AATCTTGTCTTCAAAATTATGAGAGAAGGGCAGCAATGACAGTTCAATTTACAAACAC
ACCTACAATTTAAGAAGGCCAACAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

TAGACAGAAATATTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC
CGCCTTCAAATACTGGTTGTTTACATTACACAGGTCTAAACCCTTGCATATCCCTTTATCAT
CTGTTATTTCGTGAAGACTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG
ATAGCAGTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTCATG
ATAATGAATTTTTTAAACAACAGTCACCTCATTATTTTTTCAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAATACGATAATATCTTTGGAAAATACCCAAGTAA
GTCGGTGGTCAAATTACTCATGGCAAAAAATTTACCGCATCAATTACAGGTCTCTATTA
TCCAACCTGCGCATGGGAAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT
TCAAAATTTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG
TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTTCGTCAAGTTTCATCAGCAA
TGGATCTCAAGCATTCAATACAGAAATGTTCTCTACAATAATGCCCCAAGAGTTGACGC
AGGACGTCATCGGTTCAAATCAGACCTAATCAGTAATATTTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEEFAIEGIIYACEVYDVPVPRHLHKSSTKIINAAKLIIETHLSYYTILNNI
SDIQAYLSTWLRDLGTTGPYQILSEISLMFDRTVSIFRKCTIEGGFPHLIARLYRLK
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLTIPKFNISNIIIEIFHLLDGLAFFKVNPDLSISISTASAETIFRSISEGNHQV
LELGRSLMFLLRTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKANNFNEDNNGLLIVDRNIPTDDFTLASTNRQSPPPSNTGC
SLHRSKPLHIPSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYFDHNEFFNN
QSPHYFSEHIDNNSREVITDENTIIISLENTQVSRWSNYSWQKISPHQLQVSI IQLRMGN
FIVAYDSYDNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSFYTTDHTTEAVSHSNNQDATASPLSSVSSAMDLKHSLOKCSSTIMPQELTQDVIGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTCGCAATTTATTAACGTCTCTAGTACTG
GTAAGCCTTTCTAACATTCTTGTGGTCACGTGATGTGTATGTTTCTTTTTTTTATTCCTC
CGGGTGATAACGACGCGAAAAATATTTTTTCATTTTTCTTTTAACCATCACAATTTGCGA
CGCGACGCGAAAAAATGCAGAGAAGTAAAAGAATGCTGGATAAGAAATCAACAACACAG
TTGAACATTGGCGTGCCCCGTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTGTA
TGTATGCGTGTGTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA
TTACTACTGAACAGGTCTTACTATTTTGTATGCGTAGTCTGCGGAAAAAGTAAACACAC
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC
TGGACACGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGCGGAAG
ACGAGAGTGATGATTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC
CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCATTAAGTAATA
CAGCTTTGTGACAGGGCTAACTCCAAATTTCTTGGGAAAAATTGAAGAAGAGGAAGAAGAGG
AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTCTCGTATTAAAAGGTGGTCTCCGTTCC
ATGAAAATGAAAGTGTTACTACTCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC
CTATTTCTCTCAAACAATGGAACGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA
ATACATCCTCATCCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT
CGGGCCTCGTATCTAAATGTCTATGGACACTTCGTTATACCCTGCGAAATTGAGGATAC
CAGAAACACCAAGTGAAGAAATCACCCTTAGTGGAGGGAAGAGACCATAAGCATGTCCACC
TTTCGAGTTTCGAAAAATGCATCGTCTTCTCTAAGTGTTTCCCCTTTAAATTTTGTGAAG
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT
CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCACATG
ATCGTCACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTGCATTCTAACAAGTTCAAAAAAATCAAAAGAGCAAGGAATTCGGTTA
TTTTGAAAAATAGAGAGCTAACAAACAGTTTACAACAATTCAAAGATGATTTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATATCAAGTCATCATTCAACTAGAAAGAACC
CTCAACCTTATCAATTTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAAATCTATTATTGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT
TGTCACCTCTCTTGCCATCGTGACAAACAGCAAGTGCAGAGACGCATTCCATATCTT
CCACCGATTCTTCGCCGTTAAATTCCAAAAGCGCTCTAATCTCTTCAAATAAGATATCAG
CAAATCCAGATTTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

AGTTTTCCACGGTCTACCAGGTTACGTTTGCCCAAACAAACAAAAAGTATGCAATCAAAG
CCATTAAACCAAACAAATATAATTCTTGAAACGCATATTACTGGAAATTAAAATACTAA
ACGAGGTAACAAACCAAATTACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTCCTGGAAGTTTTCAAATTCATACTATATTATGACAGAATTGTGCGAAAAATGGTA
ATTTGGATGGATTTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA
GAATTTGGAAAAATCATCGTGGAATTAAGCCTGGCTTTACGATTCATCCATGATTCTTGTC
ACATTGTGCATCTGGACTTGAAACCCGCAACGTCATGATCACATTTGAAGGTAACCTAA
AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAAGTTTTGAAAATG
AAGGTGACAGAGAATATATTGCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG
CAGATATTTTTTCCCTGGGTCTGATGATTGTTGAAATTGCAGCGAACGTTGTGTTACCTG
ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTTATCGGATGCAGGAAGATTAA
GTTCCACAGATATTCATTCTGAATCATTTATTTTCAGACATTACGAAAGTAGATACAAATG
ATTTATTTGATTTTGAAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA
CTGTTTCATAACAATAGTAATATCAACAACCTTAATATGAATAATGGCAACGATAATAATA
ATGTCAATAGTCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTCCTCG
CATGGGTACCGAAATTTCTTATTGATGTGTAATCACTTGAGAGAATAGTAGATGGATGA
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC
TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEDEEDFEMLDTENLQFMGKMFQKQAGEDESDDFAIGGSTPTNKLKFYPYSNNKL
TRSTGTLNLSLNTALSEANSKFLGKIEEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNSPISLKQWNQWFPKNDARTENTSSSSSYSAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPEPVKKSPLVEGRDHKHVHLSSSKNASSLSVSPNLFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHNRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARNSVILKNRELNSLQQFKDDLYGTDENFPPIIISSHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRKSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL
NSKRLISSNKL SANPDSHLFEKFTNVHSIGKQFSTVYQVTFQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIIMTELCENGNDGFLQ
EQVIAKKRLEDWRIWKIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGLNKLGDGFM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLDPDNGNAWH
KLRSGDLS DAGRLSSTDIHSESLFSDITKVDNTDLDFFERDNI SGNSNNAGTSTVHNNSN
INNPNNMNGNDNNNVNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECLYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCCGCATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA
GGAATGCCTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT
TGGACCTAAGCCAAAATTTTTTATATGATAAATGGAACAAAAAACCCTTGTTTTATTTACA
TACTTTTTTCCACACGTGCTTATGGGCCGCATTGTATAAATAATCCAATAACGAAAAAG
AGTGTAATTGCAGTCCGGTAGTAATACCATGTAAAACCTTAGATGAGTTTATTTTAAGTA
CAGCGCTTCAAGCATTTTTTATTTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT
TATATTATATATATATATATATATATATATCAAATACGACGTATTACATATATATTGAGAAT
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG
ATGTTTCATCTTGGTTCTTCTCCAGTTTCTTCTCTTAGCGTTGTAACGGATAGTGTTGTTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTGTCTTCTTAGCCTTAGCCATTTTT
TGCTTGATTCTGAAAGACTTTTGAGCCTAATTAAGGGAACATATCGTGCACATACGA
AGTGTAATTTGTAATAAATGTTAGTAACAATGTTCAAACATCATCAATATGATGCATTCA
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYVLRDLVHLGSSPVSSLSVVTDSVVGSDPLWQWSVLLLLSLSHFLLD SERL
LSLIKRETYRAHTKCTIVKNVSNNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTCATTTTTTAGC
TTGATTTTCAAAAAACTTATGGGCGTTTTAGGCTCCGGCTCAAACCTACCACCACCACGCG
GCAGGCCGAGGCAAAACAGTACGCCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA
GCTCAATGGTCCTTGCCTTTACGCTCGCGCGTGGGCTAACTAACGCAATTCGGCTTTTGG
GCTGTCGAGAACCGAGAATTATTCCTCGCCTTGATAGATACTTTAAACTTCTACTTAAT
ATACTTTCTACAATTTTGGTACATTCAATATTATACTGAAAATTCGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA
TGCTGAACTGATCAATAGCAAATTATAAACCACATCCATCTAAATGACCTTACCACCTAC
AATTTGGATTTGAAATAGAAGCAATGTGTAAAATATAGGGAAGGATTAGGAGTGTTAAC
CATACTAAAATTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAATA
TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT
GGTATTGCCCTTGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAATTTGTACACTTCGTATGTGCACGATATGTTTCCCTTTTAATTAGGCTCAAAA
GTCTTTTCAAGATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA
ATGGATCAGATTTGAGAACCAACAACACTATCCGTTACAACGCTAAGAGAAGAACTGGAG
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)

MAAQKSFRIKQKMAKAKKQNRPLPQWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)

TCTCGACAGCCCAAAAGCCGAATTGCGTTAGTTAGCCACGCGGAGCGTAAACGCAAGG
ACCATTGAGCTTGGAAACAGAAGGAGTCGCTTCGGCGTCCCGCCAAGGCGTACTGTTTGC
CTCGGCCTGCCGCGTGGTGGTGGTAGTTTGGAGCCGGAGCCTAAAACGCCCATAGTTTTT
TGAAAATCAAGCTAAAAAATGAAAAAAGTTAAATTGGTACTGTGCGCCCATAC
ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAACT
CAAATATTGAGGACGCGCGATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC
AATCTTTAAATTTGTAAGGTTTTTTAATGGCCTTTTCAGTTCTAGTATTTTTTATAAAACA
GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTTAAATCAGACCATCCTCCAAGGTCA
TTATCAAGTTTTTTGCAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG
ATGACCACAGATCTGGTAAGATTGTTGTTCAATTGAACGGTAGATTGAACAAGTGTGGTG
TTATTTCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAACTTGT
TGCCAGCCAGACAATTCGGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAAGCCAGAAGAAAGCACGTTTCTGGTAAGATTTTGGGTTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)

MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLQVMQKHGYIGEFEYIDHRSGK
IVVQLNGLRLNKGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)

CTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGGCGATCGCT
ATTTAAGTGTGACTTTCTTAAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTCTCTAT
GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG
CGTAAGAGATACGCTCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTCGAT
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTTCGAAAAAAGGTACGCTTCCCTGTTAT
AATCAGGTATATTTTCGTTATTCTTATAAGCTAAAAGATTAAAAATTTTCCACTTTCTCTT
GAAATTTGGTTCGGTTTCGTTGGAATAATATTATACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGGAAAAATAAAGGGAGGAAATCCTGCAGAACGTTGTTGTTTCAATC
GAAGGTTTCTTCATTTCGAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTCAATTGG
TTTATAATGAAGATCCCGATTTTACCAGATGGCACAACACCATGTGATCGGTTGGGAGTGG
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCAGTCTCAG
ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAACTAATCTTGGAACTAATGGTCAAG
ATGGAAGAATGCTTGAACAACAAGAGACGTGGTTGCTAGACTAATAGAAGAAAACA
AGGAAACGCAAAAGAGGGTGATAAAGTCTGTATTGTCCCAAGGTTTGGTACGATAAAT
TTTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT
GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG
TGGTAACTAATTTGGTTATCAACCAAACACAGGGGAGTTAGAGACAGAATACAATAAAT
GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC
AGGACGATTCAATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG
AAAAGAGTATGAATCTGTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT
TTAAAATTTGGTTTGTGTGAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT
TTTTGAATTTCTTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAGAAAC
TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC
TTGTCATAGAAATTAACCTATAGAAGGGAATCACCATTGGCCTTCAAACATTTTTGCTT
ATAATAAATCTGAACCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAATTTCTGCGTTGCAATGCCTGGTACACATTCCGCAGTTGCGTGATTATTTCTTTT
ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTTCAAGTGTGTTTCAAACAGGATGAGCATAATGCAAA
GAAATGCTGCTTTCCCTTCAATGTTTCAATCCACTATCGGGCACTTTAATTCGATGT
TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTAGCCTTCTGTTAGACAGTTTAC
ATGAAGATTTGAACAGGATAATAAAGAAAAGATACACAGAAAAACCATCATTATCTCCTG
GTGATGACGTGAATGATTGGAATGTAGTCAAGAACTGGCAGACGATACTTGGGAGATGC
ATTTAAAGAGAAATTTGTTCCGTTATAACGGATTTATTTGTGCGGATGTACAAATCAACGC
TATATTGTCCCGAATGTCAAAATGTTTCTATAACGTTTGAACCGTATAATGATGTTACAT
TGCCGCTTCCGTTGATACAGTGTGGGATAAACTATAAAAAATTTTTCCCATGAACTCTC
CACCATTCTCTTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAATT
ATGTTGGTAAAAATGTCGGGCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA
ATCAAATCTATGTTAACTATGAGTCAACAGAGTGAATGCTCAATTTTTAACCTTGCAGG
AATTGATCAAACCTGCTGATGACGTTATTTTTTATGAATTACCAGTAACAAATGACAATG
AAGTAATTTGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTTCTTTATTACGTTAAAAAGAAGATGAATTGAATAATCCAGGTGCAATAA
GAATGAAAATGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCTTGAAC
CTGTAGGAAATCGAACCAGATTTTGCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGAACAATATAAAGATATACATACAGTATACGTTCTATTAAGTGACTGACA
AGGATAAATCCTTTTTTTTCCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT
TAGTAGATTGTGCTGAAGGGTCTTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA
GTGAAGCAAAGAATTTTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAATAAAGAAA
CTGTAGCAAATAATGAAAATGTAATAATACTAATGATCGGGATGAAGATATGGAAGTAA
CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGGCGT
TAGATAAAATTAAGGATAGCTTGACTTCCACTCCGTTTGCAGTTCTTTCTATGAATGATA
TTATTGTTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT
ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA
GATCTAACGCTAAGGAAAGAACCATAACCTTGGACGATTTGTCTCCAATTATTTTCCAAAC
CAGAAATACTAGGATTAACCGATTCTGTTGCTACTGCCCTACATGCAAGGAACATCGTCAGG
CTACCAACAAATACAACCTTGAATAACACAGATATCTGCTAATTACCTTTAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTTGATGCCACGGTTAATTTCCCATTCACAG
ATTTGGATCTGTGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTTAATCTATGACC
TGTATGCAGTAGATAACCACTATGGTGGTTTGGGTGGTGGGCACTATACCGCGTACGTAA
AGAATTTTGCCGACAATAAATGGTACTATTTTGATGATTCTCGAGTAAGTGAAGTGCAGC
CAGAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTGCGCGTCATAAAGATG
GCAATGGATTAGGCAGCTCTAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGACGGCCCTG
AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG
ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA
AAGTCTACAAGAATAATTCAGGCTTGGGTTTCATCGAGTACGTTGAAATATCTGAGGGAT
GCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVYNEDPDFDTGTPCDRLGVLDLMNVLDLDDKDEIKQESVPVSDREIEDT
ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG
DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFN

LSEIYGMTSGSYPPVVTNLVINQTTGELETEYNKWWFFRLHYLTEKQDGRKRRHGQDDSIMY
LSMSALNLVRDLVEKSMNLFEEKADHLDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLELPIKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHPNSNYFAYNKLEPA
SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL
VQKLFQNRMSIMQRNAAPPSMFKSTIGHFNSMFSGYMQQDSQEFALFLDLSLHEDLNRI
IKKEYTEKPSLSPGDDVNDWNVVKKLADDTWEMHLKRNC SVITDLFVGMKSTLYCPECQ
NVSITFDPYNDVTLPLPVDTVWDKTIKIFPMNSPPLLEVELSKSSTYMDLKNYVGKMSG
LDPNTLFGCEIFSNQIYVNYESTESNAQFLTLQELIKPADDVIFYELPVTNDNEVIVPVL
NTRIEKGYKNAMLFGVPFFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEPVGNRTD
FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP
NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGVLMQVDDDEGDTGSEAKNFS
KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS
LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
TITLDDCLQFLFSKPEILGLTDSWYCPTCKEHRQATKQIQWLWNTPDILLIHLKRFESQRSF
SDKLADLWFPITDLDLSTRYVVKDDPRGLIYDLYAVDNHYGGLGGGHYTAYVKNFADNK
WYYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSKLQEI IQKSRHGYDERIKKI
YDEQMKLYEFNKTDDEEDVSDDMIECNEDVQAPEYSNRSLEVGHIEQDCNDEDDNDDGE
RTNSGRRLRLLLKKVYKNNSGLGSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167)

TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCTAGATTGTGAATAAATCATT
TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG
GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC
ATACGCATAAAGAGGTGCCTTGTCTGATAGGCGTATATGATCCTAAGCAACAGAGAAACCAC
GGTTCTCTTCTCTTCTTATTTTCGTTATTGTCTTCCCTTTTTACTATGGGTAAAGTCGCC
TAAAGCGGGGCGCTCACAATATCGCCGCAGCTACAGCCGTTTTTTTTTTTTTGTTTTTT
TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTCATCGATATAAA
GAACACTGTTTCACTTCGATGTCATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA
GTGGTAGCTGGTACAGGATCATGAGATTTTACACTTCTTGAAGTACAATGCTGTCCAG
AATGGCAAAACCATATATATGGACTACAGCGAGCTGAAAAATCTTATTTACAGCTACAAA
CAGATGAACCTTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAAGAGCTCTAACA
TTACAGATAGGTTCAAAAACAAGTTTCTTTTAAAAATGCGAAGGAAGATACGTCTTCCG
GTATGAACAAAGATGCAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCTACTG
CTCAGACGGTTCGCTGCCAAACCTTCTCCTTTTCAAGAAGATGAAGGAAAAGATATTTTACA
AAAGAAGGTCGTCTTCCGCATCGTCCGTCTCCTCCACGGCCAACGAAAATCTGCAATTAG
ACACTTATGATACGTTTGTGTTGATTTAAACAGCTGAAAAACAGAAAGTAGATGATTTTT
ATAAGAGGACAGAAGCTTCTACGACAAATTTGACGCGCTGGTGAAGGACCTGAAGA
AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAAACGAACCGATTGCCA
GCACAAATGACGAAGTTCCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT
ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTCGCAGTATAACA
TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT
GCCAGTTGAAGTCGTTTCATCGAATTGAACCGCATTTGGGTTTGCAAAAATTACAAAGAAAT
CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACCTGATCGAATCGGAGCAGTTTTTCA
AAGACACATATGCATTCAGGCAGAAACGATCGAATTGCTAAATTTCCAAAATTTCCACGC
TAGTCACATTTTATGCGCGCATCACTGACCGGCTCATAATATCTCGCATAGCAAGCAAG
AGTTGAAATCCTACCTGCATGACCACATTTGTTTGGGAAAGAAGTAACACTTGGAAAGACA
TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA
ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA
ACTTAAATTTCACTAGTATAAACAACGTTGCACTACCGAAATATTTTTTACCAAGAAAG
CATACAAGATTTACTTTATTATTCTAGTCACTGACTCTTGTAGGAATAAAGACCTTCA
ACGACGCTGCTGACACCGCTGCATGGCCCTTGTGAGTGTGTCGCTTTTGTGGGCTA
GTGAGGCCATCCCATTAACATTAACAGATTCTTGTACCCTACTTGTAGTCTTTTCA
AAGTCCTAAAAACCTCCGACGGGGCTATAATGAGTGCTGCAAGCGCTTCATCAGAAATTT
TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG
TACTTGACAAATATAACATCGCCAAAGTTCTTGCCTCGTGGTTGTTGGCCTTCGCTGGTT
GTAAACCCAGAAACGTTCTTTTAAATGGCAATGTGTGTCGTGTTCTTCTATCAATGTGGA
TTTCCAATGTCGCAGCACCTGTTCTAACAATATTGTTGTTATCTCCCTATTGGATGCCA
TGGAT
TCGGTGGTATGTCTTCAACATCTCTTCACTCAAAACATCATTTCCATGTCGATGTA
AACCTATGGTATTGGCTGGGGCCAATTTCTTGTCTGTTGCATTGCCATCTGGTATCTGG

CCATGCTTTTGGTTTGGATTTTATTGTTCACTACTTTCAAGATGAATAAGACCAAATTGG
AAAAATTTAAGCCTATTAAGACGAAATTCACAGTTAAGCAGTATTATATCATTTACTGTCA
CTGTGGCCACTATTTTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTCAT
CAGGTCAAATTGCAATCATTTCCCATCGTTTTGTTTTTGGTACCGGATTACTATCAACAC
AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTTGGCAATGGGAGGTATTGCTTTGG
GGAAGGCCGTCTCATCCTCGGGTTTGTATCAACCATTGCAAAAGCATTACAAAAGAAAA
TTGAGAATGATGGTGTTTTGGCATTCTATGTATTTTCGGTATCCTGATGTTGGTTGTGG
GTACTTTTCGTCTCGCATACAGTATCCGTATTCATCATTCCTTGGTGCAAGAAGTTG
GTGACAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTTTTCGGTTGTGCATTATTGT
CATCCTGTGGTATGGGACTAGCTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAGGGCGATCGCTATTTAAGTGTGATGACTTCTTAACGAGAGGTGTTCCAG
CTTCTATTTTGGCTTTCTATGTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTG
TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAVPEWQNHMYMDYSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN
KFSFKNKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRRMKEKIFYKRRSSSA
SSVSSTANENLQLDYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPPDLDDDDDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS
LLKKSIVNLYIDLCLQKSFIELNRIGFAKITKKSQKVLHLNTRTELIESEQFFKDTYAFQ
AETIELLNSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTPKETEYNANKLVGKLDLEYRWPLPRPINLKFTSINNVALPKLFFTKKAYKIYFI
ILVTGLLLGIKTFNDAAQHRCMALVECVAFWLWASEAIPHLITAFVLVPLLVLFKVLKTS
GAIMSAASASSEILAAMWSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNVL
LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP
ISSPQNIISMSYLPYIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK
TKFTVKQYIIITVTVATILLWCVESQIEGAFGSSGQIAIIPIVLFFGTGLLSTQDLNAFP
WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVSHT
VSAIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTAIKVDKRGDR
YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATTCTTTGAAAAGATTATTAAGTTCGTCTGTTAAGTTCCGCAATCT
GCATTTTCATTTAAAGACGGATCATATATTCTTGTGCTTTTTTGTGTTTATCTCTTTACTTA
CTTGTCGCTTCCATTTCGTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCCCTGGGCC
TCTGGTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGTGCTCTTGAAATC
GTACCGAAGTGAAGTTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGGCCTTGGCATATAACGGTGTGTCACTTTTATTTGCTCTTTTCATG
CATCCTGAAATTATTTACCCGCACTACGCAAAGAGAACGGAGAAAAAGGTATAATAGGGC
AAATGATCATTGACATCGTGATCGTAAGCAAAAAAATAACAATAGGCTCCCTAAATAA
GTAGAGTAAAGCTCTTGAGATGAAGGAGAATGACATGAATAATGGCGTAGATAAATGGG
TAAATGAGGAAGATGGTCGAAATGATCATCATAACAACAATAAATACTTGATGAAGAAGG
CCATGATGAACAATGAGCAAATTGATAGAATCAGGATATCGACAACGCCAAAGAAATGT
TGAGGAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTTCAT
CTCTCGTGAACGGCAATGCAAACAGTGGCGGTGGTACGAGCATTAACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTCAGTATGCCTCCACGGCGTATGGTGTAAGAATGT
TGAGTAAAGATATATCTAATACCAAAGTGGAACTGGATGTGGAATTTGATGATTGTTA
CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTTGG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG
CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA
AGGATTTTCATCAGGGAACATGATGTTTCTTCGATTTGGTAGTGACTTTGGGTGGCGACG
GTACTGTTCTTTTTGTAAGTTCCATTTTTCAGAGACATGTACCACCCGTTATGTCTGTTT
CATTAGGGTCTCTAGGATTTTTTAACAAATTTTAAGTTTGAACATTTACGGGAGGATTTAC
CTCGGATTATGAATCATAAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAATTT
ATCGTAGACACCGCCCTGAAGTAGACCAAAACACGGGGAAGAAATATGTGTGGTGGAAA
AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCCTTTTC
TATCCATGTTAGAATTGTATGGTGACGGCTCATTAATGACCGTTGCGCAGGCGGACGGAC
TGATTGCTGTACTCCGACTGGGTCCACGGCCTATTCTTTGAGTGCAGGTGGGTGATTGG
TATGCCCAACCGTCAATGCAATCGCTTTAACACCCATTGTCCACATGCATTGATTGCA
GACCATCATCTTACCAGAAAGTATAAATTTAAAAGTGAAAGTCTCGATGAAGTCAAGGG

CTCCAGCATGGGCGGCTTTTGATGGGAAAGATAGAATTGAATTGCAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA
TTAACAGTATCAGTCGACAACTAACTGGAATGTGAGGGAACAACAAAAGTCCTTTACGC
ATATTTTGTCCCAAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC
AAGCAGAACCCTTTAGAGGTAATAAGAGATAAATACTCTCTGGAAGCAGACGCTACTAAGG
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAACCTGCCAAGCTTGCA
AATTAAGCCTTCGAGCGTCCCAAAACCTTCTCAAGCAAGGTTTTTCAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNNGVDKVWNEEDGRNDHNNNNNLMKKAMMNNEQIDRTQDIDNAKEMLRKISSE
SSRRSSLLNKDSSLVNGNANSNGGTSINGTRGSSKSSNTHFQYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRELVEWLVHFPRTVTVYVDSSELKNSKKFAAGELCE
DSKRESRIKYWTKDFIREHDVFFDLVVTLGDDGTVLVSSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRLRLECTIYRRHRPEVDPNTGKKICVVEKLSTHHI
LNEVTIDRGPSFPLSMLELYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMKSRAPAWAAFDGKDRIELQKGDFFITICASP
YAFPTVEASPDFINSISRQLNWNVREQQKSFTHILSQKNQEKYAHEANKVRNQAEPLV
IRDKYSLEADATKENNNGSDDESDDSVNCEACKLKPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:
877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT
AACAGCGAAATTTATGACATATTATTTTGAACCTTTTACAACTAGTAGATTTAGTGATT
TATTACCTATTGGCATTCAATTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT
CATCGGAGGCCATATCATCTTTTCGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC
TAATAGATTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTGTCTGAACTTTTTTTTTTT
TTTTTCATGTTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT
GATCCGCCTCATACTAGCCATTACCCATCTATCCCAGGCATTATGGGTATGCAACTCATA
ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTCCCGTTCAGCAAGAGGT
AAAGCCACCAAAGGTTCAAATGCAAATGTATGTTACGGCGAATACAGAATACTATGTTT
GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA
ATGATTGACAAGCTCACAATTTATTAACAAGTAGCAATTGAGAAAACTATTACTCGCG
GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAATTGAAAATGTGCGCATATGTGCTG
AAGGTTTGTGTTTCCATCTTATTTGCATAACATAGTTATATTTACTTGGTTCGCATAA
AAAATATTTTTTACTAACGTGAAGTTCTTTCTTTATGATGTACGCACGCACGTCTGTGC
TTACTCCATAAATGAACCTTATTTCCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA
GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA
AGACAAGGAAGGTATCCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA
AGACGGTAGAACTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT
GAGATTAAGAGGTGGTATCATTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACCTG
TGACAAATCTGTTTGTGCTAAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG
AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTTCAGTC
AAGCCATGTCTTTACTTCGTTTTAATGTTAGAAACAATCGCTTATTTGTTTTCTTAAACA
AATATATTAGGTTCAAGGTCTTCGCAGGTGTAAGAAAACCCGTGGTCTCCATATTCTTAA
GTATGATAAATAAAAAAACTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTTT
TAGTTTTTAATATTTCAAACGTTATCTTCATTGAACGCCCAAATAGGGAAAAATCCTGGC
AAATTTTTTATTGCTGTCTATCCAAGGCTATGCTAGAAAATTCAAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTATTCTTTGTTATTCTGCTTTACCTGATCATATT
CCGGCGTATTGTTTTCTAATCAAGTGATTTCGATATCCAGTTACGAACCATTTACAACATT
CCTGAAAATATTGCGTATCAATGATATTTGCTCCTTCTTTCTCCCTCATTAATAAATATTC
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTTGCTGCCAAAACCTTTAACGTCTAGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTCTTCATGGAGT

TTTTAAACGATTTTCGACACCGCTTTTCCACAGTATACCTCATACATGATGCAAAACCATT
TAACCCTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG
CAGATTTACAATCTGATATTGCTCAGAGTTTTCGTTCACTCAATTCCAAACATTCATTA
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAATTCTGTTCTCTTCTCGACAGCGAACGCAGGCCAGTCCATGA
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACCTCTTCTT
CAACATCCAGAAGTAGTCAATCACAGAATGGTCCCCATGCCAAAAGCTTATATTTCCCCA
TGGCGTTGTTTCGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)

MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDDTLARSAAADADMAFFMEFLNDFDT
AFPQYTSYMMQNHLTLQPQVADYHHMVDLASTADLQSDIAQSFPFTQFQTFITAFPWYT
SLLNKASATTIYLPQHFIETGETEATMTNSSYASQKNSVSNVSPFSTANAGQSMISMANEE
NSTTALISANSSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCCTTTTCTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTCAACACTTTT
AATATTTCCCTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT
TACCTATTTCTTAAAGGCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC
GCCTACTTTTGAAAAATTTACCAAGGCGAAATTGAGTGCGCTAGGCGGAAGTTCCAGGGCA
CGGTCACCGAACCTTTGTGCTGTTTCGAACGAGGGTCCCGCTGGAGGTTGACGGACGCGG
GAGGAGCTGGAAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCTGTGGTAGG
GAACATCACCTTCTCTAGTTCCTGTAAAATAATATGATCAAGTTTGAATCCTCGTATTG
AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAGAAGAGATAA
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATTATAAGGTCTCGAAAAGAATATGTCCCCGA
TTTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTAGAGGAATTTGAACACGCC
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG
AATATACATCCTCGACTGTGTCAAAGATTATGAACTCCGATGAAACAGTAAACGTCAAA
AAATTCACGGGATATAATTCGGTACTTTATTGGATATGGAAGAAAACATTATATATGCA
CAAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTATAGGTCCACCAAGA
ACCATACGTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG
GGAAAAGTTGGTTTGGCTGCTAGAATTATTGCTGCCATTCCAAACCCAGAAGATGTTGT
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG
TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTT
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA
ATTTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTAATCTG
GTACTTGTGGCTAGAGAAGTTTGGAGCTAAGAGGTGCTTTGGTGCACAGAAGTCAACC
ATGGTCCATCATGCCAGATTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGTAAGGAAGAAGTCACTGA
AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)

MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIPNPEDVVAISSRTYQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDPRLDAQAIKEASYVNIPIVIALDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTPQWSIMPDLYFYRNPEEVEQVAEEAAAEEGEEEEVKEEVTEGQAEAT
EWAEENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)

CTTCCCATGTAGAATATCATTTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT
TCCATGCTTGCTAACTTATTACCGTCAATAGAAGCTTGAGTCAGGTGGCTTTAATGAGT
ACTATTCTTTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTG
AGTATCCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAATACACGC
CGGCTACACTTAGAAAGAAATGACATTTGCTGTCTTATAAAGGACTTGACAGACCAAAG
ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGCGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT
TTGGGTTTATTTCTATAGCTATTCTGCCTATGGATGGACAGTACAGAAGAACATACATTT
CTGAGAATGCATTGATGCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TTTTGAGGGGCTATCGATCTCAAATTAAGAAATGGTAAACATGACTTCTATGGAAAGAA
ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG
AACAATATGGAGAAACATTGTACGGTGTAAATGCACGCTCCTAGGGGTGATGGAACAGAAG
CGATGGTGTCTGCCGTTCCATGGTTTAATTCAGATGATGAATTCAATATTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA
TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAAGATCATGGGTTGAGGCATACCATA
CTTCCTTAGATTTGACTGGTGGTTCCATTGAAGCTGCTGTTGTGTTGGATTATTCGAGTA
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATAACGACGGTCTGAATGGTGAGCTGCCCA
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT
TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAAAAATAT
TATGCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGGTAACGAGG
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAAACAGTGGTCATG
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG
AAAAATTTACCAATCGTTCTTCTTTATTGTTATTAGCACCACGTCAGTTCGTATCCA
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTGCCATAAGTTCATTAA
ATGCATTTATAACAATGCTTATGCAATATATCCTTATTTTCCGAGTATAATTTGGTAG
CGTTGTTGGTTTGGTTCGTGTCATTGGTGATATCATTGTTGTTTACAAAGCGTTTCTTC
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCTATCATAACAGGTTGAAAAATGTTGCTT
TTTTATATTTTCACTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC
TGATCGGCACATTGGCATTTCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG
AACATGAGGTGACAACCTCAATCCTCTAACCCTAATAAAAACTGAGCCGAAAGATGAGTAG
AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAAC
TAAAAAATTTAGTACTATTAATTTTGACAAATCCATTTATTTCAATAACCTTATTCGGAC
TATTTTTTTGATGATGAATTTTCATGGATTTGATATAATAAACAACTGGTTTCAGCATGGT
TGGATTTGAAATGTTGGAGTTGGTGTGACTTTGTATAGGTTGGCTTCCATGTTGGCTAT
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCTAGTAAGGTCGAAAGAAAAGCAAA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIALLPVISMALCALFGFISIALPMDGQYRRTYISENALMP
SQAYSFYFRESEWNILRGYRSQIKEMVNMTSMERNNLMGSWLQEFGTKTAIYENEQYGETL
YGVMHAPRGDGTTEAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIVVFSN
PRAALRSWEAYHTSLDLTGGSIEAAVLDYSSTEDFFEYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVSLSHGLPSDQLTNNNFWSLRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGNSGHDITTFGRIPeamFRSINNLEKFHQSFFFYLLAPRQFVSISSYLPS
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLIPSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFLVSTSLLMINFAMALLIGTLAF
PMTFVKTIVESSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLNVL
ILTNPFISITLFLGFFDDEFHGFDIINKLVSALWDLKCSWFVLCIGWLPCWLLILASSF
ESKSVVRSKEKQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTCGCATTTTACTATCCCCAGTTCCG
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGCTCACAAGGCGGTATGACGTTT
TTAGCAATGTAATTATATTAAGGATCTTCAGTCACTATGAGTGGTTGATTGCCCCATA
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCAGCTGGCTCATGTCTGTCACCAAGT
ACTAGTCACTTGGTCGCATTCATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCAAAGGATTAGAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTTTTTTTTCTTATTTGGTGGCGAAACAAAGGTGATGAAG
TTTCTTCTTGTACAAACGCCAAGCCCGATAGGTGAGACAATCTTGAAGTAATGAGACCTC
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCTAGGCA
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTAAACACCACTGGCTTCCGGAATACT

ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAAA
CTACAATCATATCTTGTATGCGGCCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG
AGACCCTCCGTTTCGCAACCGTGTCTCTGTTTTCATCACTATATGCACGCTCTTTCCAAA
GCTCCTGCACCTTTCACAGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)

MKFQYALAKEQLGSNSRSGVKKLISKHHWLPEYYFSDLSFSVQWDSRAIEKTTIISCM
RPNQEIYPLRHCETLRSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMVGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)

ATCAAAAGAGTGTTCAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAATAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT
ACCTGGGGTTAATGAACGAGAAGTCTTTGAGATATCTTTCCCTGTTTACCTCCGTGCATCC
TGTAAGGAATTGGGTTTATCATTTATCATTTATTTTAGTACAACTTTTTTTTTTGGCCC
GGGCGCACTTTTTCAAGCGGTGGGAACCTCATCAAAATGAAAACTAGATACTTTTAGACT
TATTAAATGGTTTTAAATATTTTGAGATGTTCTGTTATATCAGAACTTCCTTACTTCTATC
TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT
AATTTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG
AAGGTATTTCCACCTGACCAACAAAGATTGATCTTTTGGCTGGTAAGCAATTGGAAGATGGTA
GAACTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA
GAGGTGGTGGTAAGAAGAGAAAGAAGAAGGTCTACACCACCCCAAAGAAGATCAAGCACA
AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCTTACTACAAGGTGATGCTGAAGGTAAGG
TTACCAAATTGAGAAGAGAATGTAGCAACCCAACCTTGTGGTGTCTGGTGTCTTGGCTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATCCGCTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGGKRRKKKVYTPKKIKHKHKVKLAVLSYYKVDAEGKVTKLRRE
CSNPCTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)

AGCCACCAATTCCACCAGGCCCGGCATTCAAGTACTTGTAAGAACACCAACAGGCAAAGT
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC
CAACCAATATGTTCGGGGAATTGGTGGGCAAATGAGGTGATTCGGCCAATATCGAAATATT
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTTACCT
CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATTCTCAGGTTCCGAAATTCCATGAATTTGCACTGGTTGTAGAAAGCAT
AATAGTCTGATGGAAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT
TATAAAACGTAATTAAACAATGAATTCAAATTTGCAGTGAGACTATTCAATTACTGCAACTT
CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGAAGAATAGGTAAGTCAATGCTGA
CCCAAGGCACCTTTCTCTGGCTTCTTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT
CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA
AAGAATTTCCCGCATAAGTACGTCACAGGCTTATCGTCGGACGATAGTCCCATGGATTTAA
ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCGGGATATTCTCCGTCTAATTCCAAAG
CTTTCTCCATAATTACCAGTTTGTCTTTTCTTTTCCACAGAATATTTAGGCTTAATATGTA
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)

MGASSGRIGKSMLTQGTFLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLGICTY

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)

GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTTAGGTGCCCTGCA
ACACTAGTCATGGTAACTTCGAGTTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCCT
CCTAGGATCTGTGAAACTGCCTTCGCTATAGAATTTTCTCTGCGACACATAGCACTTTC
ATTATTGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTC

AAAAGCGATGCCCTCTTTATTGACAGTTACTAATTCGCCAAACTGCTTTTTTTTATCAAT
GTGATTTTCGCGTTCACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG
CCTGTATGATCCGACCGTTTGTAGCAAACCTTATCAGGGGAAAAAGTATATTCCATTAAAT
GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG
AAAATGCATATATCACGTTTCTGATGCTTCTGATGGAATACATCGCAAATCTACTAGGT
TTCTCGAAGAGCTACTTTTGAACAAGAAAAATATGTACCATAATAACAATTACGAACGCA
TAAATGATTCCGTGATACCATTTGGTTCTGAACTTTTATGGCTTCAAATTCACGAACCTA
CACTCCAATGGTTTGGACACTGGTTCCATGATATCATGCGACTAAGTAACAGAAGAAAGT
TCAGAGTTTTTAGAATTTTTCAAAAAAAATGATTCAATTTTTTCAAATTTACACACAGGT
ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCGGTTATTTCAA
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT
GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGCTAACA
AACCACAGAGTGGGAAAGGTTTGAAGAAGTCTATTAGGTACTTGAATATTGCCCTCACTCT
ATCTCCAGCCGTTGGAGATACTTATTTTTCAACGAGCGAAAATTTACTTTGATCACTGGGA
AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTGGTAAGGATTCCGCTCAAAT
GTGCGTTAAACAATTTGAAAGATTTCAATTTTGACTCCTGATTTTCCGGAAGAAGACGTC
TGATGAAAAAATTGGCAATTCCTTGCTGCAAAAGATCTCAAAGGTGAGAAATCATTTCTTG
AAGGTCAAATTTGTTTGAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT
GGAACGCATCACGTGCTTCTAATTGTTGGTTATTGAAAGAGCATTACAAATGGCTGCAT
TAAAGTATCATTCAGGTAATATTAATGTTACTTTGAAAACCTGGCTGCCACAATGGGAA
GTTTCGATCTTATGTTTACAACCTCGAAAAAGTAAGGAACAAAAGAACAACACTCAAATATG
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA
TCATAGACGTCGTCATCAAACCCTCCTGGCAAAAAAACATGGAAGACTTTGATATCTAG
CCATTATTCGTTTGCTTATGTGCTGGATTAAAGTCATATAGATCTATTTTGCAGTACACTC
ACAGACACAGGAAGTTTTGCACTTTCATTGCGCTTGTTGCTGAACGACTTGATAAATAGTC
CACTGAATTTGTTTCAAGGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTTAGAG
AAGATATTATTTTCAAGGAAATTTTCTTGCACTTAACCTTTGCACTAACAGATTTAATGACG
ATTATGTGTATGATTCCTCCGACATGATTAATAATATAATGATGATGCTTACATGACTA
AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA
TGAAATTTTTTAGAGAAAAATGACACCGGCGTCATATGGAATGCCAGCAAATATAAGTTTG
ATTTAATAAGCCCAAATATTAATAAAACGCCAAATAGCATTATCGGAAATTTCTCTCA
AATAAATGTAAAAACACAACAGGAAAAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA
GAGATGAACAACAGCGCAAAAGAGCCGGGAAAAATAGCTGTGACAGAACTGGAAAAACAAT
TTGCAAAATGTCCGGAGAACAAAAAATGTTCTCCGCTCCAGAAAAAGATGGCGTTTCTT
CTGAGTTGGTAAAAACATGCTGCTTACGAGGGGAGAAAAACTATCACTGGCCCACTCTCT
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG
TGCCAGATACTCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)

MDNEEVNEECMRLFFKNARAHLDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL
KQENMYHNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIIIEHLCAKYDMNSVISNALFAKLNLQMQYTDGLSTHEKII
NPLTFSIVISLQRCVINLGSTHFYKTLNKPSPKPKSVEGFESIRYLNIAASLYLPAVG
TYFQRAKIYLLITGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRRLMKLAI
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVPSQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSFDFLMFTTRKSKEQKNKLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILOQYTHRHKFKTSFALLLNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDNFNDYVYDSPDMINNIIGCPTLTKVLSPE
ECVLRIRSIIFSGMKFLEKNDTGVIWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASGRKTTITGPLSSDFLSYPDEAIDADEDITVQVPDPT

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCAGGAATCATTTATGCGTTCGTAATTGTTATTATGGTACATATTTCTTGT
TTCAAAGTAGCTCTTCGAGAAACCTAGTAGATTGCGATGTATTCCATCCAGGAAGCAT
CTGAACGTGATATGCATTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA
TGCGCACGAGCGTTCTTGAAAAATAATCTCATAACATTTCTCGTTAACTTCTTCATTATCC
ATTATCTATGGTGGCATGTGTCAATTAATGGAATATACTTTTTCCCTGATAAGTTTGCT

CTTCGTTACACTTAATATTAAATAACAGCTCTTTCTTAATAATAACATATACACTAGAT
ATATAATACCAAATAAATTAAAAAAGAAAAACAAAAATAACGTAGCTTTGTTACAG
TCGTAAAAAAGAACAAATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCATTATAT
TCCAATATATTAAGGGGTAAGGACTACTATFATTCGCCCTGAATTGAAATCTTTTAGAAA
GCACCTGTTCTCTCTCTGGTGTTCTTTTTTCTCATCTATTATCTAATTTCTTCAACCTT
CGTTATTGTTGTTATTCCGTAATCGTGTTGCTCAACTTTTGAATTTCACTTGTTTACC
ATAACGGAACATAATAAAAATTTGTTCTTGAAGTCACAAGCACTACGTGAACAAAA
TTAAGGCAAGAGTGACAAAGTAACCCTCACAAGGAGCCTGTCGTTGGTTATATTGGAAGC

TATAGATATAATCGAATCCAATGACTGGTCTGACCTGAAATAAATAAGGAGGAGCACC
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAAATATACTT
ACATTCTAGTCCCTCACATCACTAAATGGAACCTTTTGAGAGCAAACATGTGGTGATACCAT
TTAAACCATGATGGTTTGAAATTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAAGAGTGGATTACACACACTTTTCCCAAGTAAGGTCCGATA
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC
TCACGGGTAAAGGTATATATACGAGACTTAAATCCAGTAATGGTACGTTCAATTAACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGAACAG
ATATAGATACGAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAACTATTTGTAC
AACCTTTATTAGAATCACCGATTTTGAAGATGAAGATAGTGATGATTGCCATACAATTA
CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG
AATTGGAAGAAGTTATCCTGGGCTCTGATACAGAAATAGTACTGAGTGGAAATTTTATTAATA
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC
CATTTTCCAAATGCGATAATTTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA
CGACACATCTAGAATACACGAACAACTTTTAGTGGAATAAATGATCAGCAACTGGTAA
AGCTGCAAAATGGATTAGAAGGAACTGTCTGGGGAATACGAAAAGATTATCGAACAAA
ACAGAAATCAAGTAAAACAGTTGGAAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG
TGAAGAAAGAAGAAATAATGAAAAGCAAAAAGCATGGAAAGGGAAATAGAAGACTTGA
AACTAGGTTAGAAGTGGAACGATATAAGAATTCACAAATGATGAAGAAGAACAAACAGA
AAGAACAAGAAGCTCTCAACTGCATCTAAAAAAGACTACCGAACATGACACTAGAGGCG
TCCCGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACTATTAACATTTGGAACATTTCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKEEHPSSPGKKQITYNSIPKNaNLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYTYILVLTSLNGTFESKHVVIIPKPDGLKLGRPVANSNSSSSSLRGGK
RVDSTFSQVRSDNGNFDNRVLSRNHALLSCDPLTGKVIYIRDLKSSNGTFINGQRIGSND
VEIKVGDDVIDLGTIDITKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLEEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTHLEYTNKLLVEKNDQQLVKLQNLRLRRLSGKYEKII EQNRNQVKQ
LERDHMFKKSFVKKRRNNEKQKSMEREIEDLKTRLEVERYKNSQMMKKNKQKEQELST
ASKKKTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT
TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTTCAGAATCTAATCAATGATA
GTGTAAATGCTTTGCTGCCTATCGTGATTGATCATTTACATAATCTGGCACAATACTGGC
GGACCTGATTGGTTGATAATTGGTGCTTCAAATTTAAATTTTCGTCACTCTAATTATACT
TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT
AATTTGCACTTTTTTATTTAAAAATAAAAAATCACAGTTAATTTTTTCATGATCTTGCAAA
GACACGCCTCCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT
TAACATAATGGCGGGCACGAAGGCTAAACAAACAAGATTAGCATTGAATGCCTTTTTTGG
GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
ATCTTGATACAGTTCAGATGAGCATCATGATTTAGAAAACCCACCGCCAAGGTTGTAA
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTGCTTTGCTTTCTGTTCTCAATTC
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC
GCTTACCGTCTCTGGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTGTATAAGATAC
GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTGTAGTTTTC
AAATGTGCATCAAATTACTTTCTATTTTTTGTCTTCTCTGTGTGCGTTATATCTCCAG
TAAGATATCATTTTACTGGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAAGTT
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTCACATATTTCTTCACCT
TCATAGCAATTAATGGCAGTTGCGGAAACAAGCACGTCGTAAGTACTAGGCAAGCTT
ATCTTGGGAAGCAAAATACGATTACTGATAGAAGCATAAGGCTCTCAGGCATCCCGTAG
AGCTTCGTGATTTCGGAAGCCTTAAAGACCAGAATTGAACAATTAAAAATCGGCACCGTTT
CATCAATCACTATTTGTGAGAGTGGGGTCCTTTGAACAAGCTATTTTATTGTGCGGAAGA
AAATACTCAAAAACCTGGAATTAATAATATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG
GAGAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT
CTCTTGGAGAGAGACCAAAAATGAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG
ATGCCATAGAGTACCTGGAGCAGCAATTAATAATTTATTGATGCTGAAATTATTGAAGCGA
GGAAACAACACTACTCCGCAACACCTACGGCATTTCGTTACGATGGATTCTGTTGCTAATG
CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG
CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTAA
CAAAAGTTTATTCTACTACCGTATTTATAGGCCTTTCAAGTTTGTTTTATGTCATTCCTG
TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTCGAAATTCTGGCCAAGCGTAG
GGCAGCTACTAAAAGATCACCAAGTGGGCCGCTAACATTGTAACGGGGCTATTACCAACCT
ATCTCTTCACATTGCTTAACTTTGGAATCCCTATTTTACGAGTATTGACTTCTTATC
AAGGATTGGTATCATAACGGAAGAGGAAATCTCAGTTGTTTCAAAAATTTCTTTTATA
TTTTTGTCAACCTTTTCTTAGTTTTCACATTGGCAGGTACAGCATCTAATTACCTGGGCGT
ACCTCAGCGATACCACCAAAATTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT
TATTCTATGTCGATTTGATTATATTGCAAGGTATTGGTATGTTCCCGTTTAAAGTTGTTAT
TAGTTGGTAGTTTGTATCGGCTTTCCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC
GGAATGAACTTTACAATCCACCGATATTTAACTTTGGACTACAATTACCACAGCCAATTC
TGATTTTGATTATAACGTTGATCTACAGTGTAATGAGCACGAAAATTTTGACTTCAGGGC
TGGCGTACTTTATTATTGGGTTTTACGTCTATAAATATCAATTGATTTTTGCCACAGATC
ATTTGCCCAATTCTACAGGAAAAGTATGGCCATTAAATTTTAGAAGAATCATCGTTGGAT
TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTGGAAGGAGGATGGGTTT
TGTCATCTTGCCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTTATATGATTTGAGA
AGAATATTTGCCGTTGTCAAAATATATCGCATTGAGTTCAATTCGCGAGTACGAAAGAG
ACAATTCACGGTGAATTCGCCAATGAGGAAGAGTCGTATGCATACCCTTACGCTGTGA
GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAAASYLDTVPDEHDFRKPTAKVVTTQLTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSLFGWLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDGNDDDDSESLIHLVKRIVEGSGDGNHSAPERTNV
YLWMYVLFTYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRTIRLSGIPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLHCRKKILKNLELKYSECPRELRTROPYSENY
HLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEII EARKQHYSATPTAFVTMDSVANAQMAQAVLDPRVHYFITRLAPAPHDI
KWDHVCLSRKDRLTKVYSTTVFIFGLSSLFLVIPVSYLATLLNLKTLKSKFWPSVGQLKDH
QWAANIVTGLLPTYLFTLLNFGIPYFYEYLTSSYQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQGIGMFPFKLLLVGSLIG
FPLVKIKAKTPRQRNELYNPPIFNFGQLPQPILILIIITLIYSVMSTKILTSGLAYFIIG
FYVYKYQLIFATDHLPHSTGKVVPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSSCLFP
LPVVTLCLFLYDFEKNYLP LSKYIALSSIREYERDNSTVNSANEEESYAYPYAVSELEGPM
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)

TTCAAGTGCACCTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT
TATTTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAGGGCACCAATGCTTTATATGC
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA
AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAATACACGCACCCGATGCTAATG
TACAGGAATTATAGAGCACATGACCCATAGATTATCGAGCATTGTTGCAATTTGCAAAG
ACTCTTTCACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTG
TCTACTAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA
ACTTAGAAAATACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAGAAAGA
AAGGCACATAGCAGCACACAATGTTCGCACCAAAACCAGCTTATTCACAAGCTTATATTT
CTAACTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCCATCTTTACAATGGCTC
AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC
TCTTTGATGAATTCATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG
ATAATGCAGTGTCTCATGAAAATACTCCGCACTTACAAATGGTGTACCATTGACCGGTT
CCGAATACAATGTCCTAGAGAACATGAATGGAGCTGATAGTATTATCTCTAACAACAAT
ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG
CCAGCAATGGTCCGAGCAACAAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCCTAAAATAAGAGATA

CTTTCATTAACGGAAAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAACGCCAATTCTGGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACATATGG
GTCATACCATAAAAGACCAGTTTCTCTGGAACACAATGACGACTCCATATCTCCGGAGG
AATTTGCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAAACTCAAA
TTGCGAATATAATAAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTTTGAAG
ATAACTTCCAGTGGAACTTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA
TTGTACAGGACCTTGGCTTAACAAGAGAGTTTCATCCCCTTAATATCTCAATCGCTTCATG
AACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTCAGGACCATGTCC
CAAACGATGCCGCATTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACTGGGCT
CCAATTGGTGGCCAAGGGTGGAAATATTAACAAAAGAAGAAATACAAAAGAGAGAAATTG
AAAAGAAAGAACTTAAGAAGATTGAAAAGAGAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCACAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)

MSHQNLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNYAEYDNDLFDEFNM
NGSNFNNADTHYKDNAVSHENTPALTNVMTDGSSEYVLENMNGADSIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHNPFFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDSSISPEEFASIYC
KDLDMTSATLQTIANIIEQLKDLLENIAATEIMSDLHVIINLTCNLQDRFFEDNFQOWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKKDWVDGHLIQDHPNDAAFQ
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRRLLKRETDRLSRRGRRLDDL
ETMTRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)

GTCATATCAAGATCTTTACAGTATATAGAGGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCCAGAGAAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCCTCTCCAGAATTGGCGTTTGGCTTCGTTTCTTGATCAGTGTTG
AGTCTATATGGAGACACCACTTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATGTTGAAGGGGTTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA
TCCTGTGCCTGCGCTTTGTGTGCTCGGACCATTGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCCACAACCATGTTTGAACCCGCATCGTATTTGTTGTTAGAGATAATACTA
TCAGCTCCATTCATGTTCTCTAGGACATTGTATTCCGAACCGTCCATGGTAACACCATTT
GTAAGTGCCGGAGTATTTTCATGAGACACTGCATTATCTTTATAGTGTGTATCAGCATTG
TTGAAATTAGAACCGTTTCATATTGAATTCATCAAAGAGATCGTTGTCATATTCCGCATAG
TTGACCACTTTAGCCCTTTTATGCTGCCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTTGGTGCGACATTGTGTGCTGCTATGTGCCTTTCTTCTTTCTTTTCAATGTAC
TTCATTCAATAATCTCTATTTGTGCTGATTTTCTAA

YLR322W, 104 aa (SEQ ID NO 196)

MRHCIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDITIFVCQ
SVMKVRNISLWNKLVLVRHCVLLCAFLLSFFNVLSHSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)

CCACATGTCACAACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA
GCCTTGCCAAATAAACTCGCTTCCCAGAAAAGACGCCAAATTAAGTCCCGCTGTTATGTG
ACAAAACAGGGCATCTCACATATTCCGCTACTGGTGTCTTTTAGCTCATTTCCGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAACCCACACA
ATTAATAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA
GCATCATACGTTTCGAGTGGAATAATTATGGAGAGTTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGCACAAATATTGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAAATATTTCAACTGTAGTTTTTTATTTTCAAGTTGAATATAGTA
CGACAAAATATCAAGGAAAATGGCTAGAGAAATCACCGACATCAAACAATTTTGGGAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAAACAAAATTGAACAAGG
CCGGTAAGCCATTTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTGTACACTT
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKTATVKINKKLNKAGKPFRTKFVKVRGSSSLYTLVINDAG
KAKKLIQSLPPTLKVNL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)

TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA
TCGATTACTTATGCTATTCTATTGTATTTGAGCCGGCGGCTAGTAAACAAGACAGCATAC
CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTTCATGTAATGTATGGGTT
AACTAATCCTTTCTCTTCTTTTCTGAAAAATCAGTAGCTAGAGGAACCTGTTTC
GTGAAAGATATGGAATATTCGGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG
GATGGAATCTTGCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCATTCTATATTATTGACGTA
ACCAACAAAAAAGTATCAGAATGGCTAAACAATCATTTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCTGTAGAGCTGGAATTGAAAAATATAGTTTGTACCTTTTGCCTGAGGGCAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA
CTTGTAAGTATTTAGGTGATGTCTCATAACTGCAACCACTGGAAAATGACGCAAATATC
AAAATAATAGGGAGATAAAGTCTCACGACATGAAAAAATCATAGAATTATTGTTCAATTT
CTTAGCCGTATCTTACCTTATGGAAAAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTTCTCCAAGG
TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTCAACGCCCATCCT
CCCAACGTGCTGTTTTGCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA
TCAAGGCCTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTTCGTGGTTCCAAGAAGG
GTCAAGAAGGTAAGATTTTCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAACCTGCACCCATCCAAGCTTG
TCATTACTAAATTACATTTGGACAAGGACAGAAAAGCTTTGATCCAAAGAAAGGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)

MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKALIQ
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)

ACTTTTGTCTGCTGCTGGTCTGTTTGTCTTTTCGTTTTTAAATTTGCGCTAGACAAGTAAAC
AGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCTCAGTTGTGGG
CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCGGTTGAACT
TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTACGCAATTACAACCGCATT
ATTTACCTTTTTCATCTTTCAGTTTACGGTTTCAGTTTATTCTGTTACGAAAGAACTATGGT
GATTCAAAGGCGAAGTGCGTAGGATTGTAACCTCTATATCTTTAGGATACCTTACAATTTT
GTACTGTTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA
TTTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAAA
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA
TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAACATTTTTTCAATATTT
TCACATGTGTTTCAATTTCTGCTTATTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA
ATGTTGCGCAACTCTAACGAAGAAATAATTATTTGCCATTGTTTTTTACTCCGGGCTGATA
ACTAGATGGTGTGATCGGGCAGTATACTAATTTATACTGGACAAAGACTCGTAAAAGATG
TTCTTTGTGCTTAGTCCCATACTGTTTTTTAAAGTGTCGGGATATTTAATCCCATGTGGA
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
TACTTTTCTCATAAATCTCACTCTTAAATTTTCAATGGCAAAATTTCTTCCGCACAACCTT
AGACAACATTTTCTTGTTTTTTATGAAGTAAGCAAAATTTTCAATCAACAACGCTCCAT
GAGATTTCTCACTAACAATTTACTCCTTATTAGGTTACATTGGCGAATTCAATACA
TTGACGACCACAGATCTGGTAAGATTGTCGTTCCAACCTGAACGGTAGATTGAACAAATGTG
GTGTTATTTCCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCAACT
TATTGCCAGCCAGACAATTTCGGTTACGTTATTTTGTACTACTTCTGCGGGTATTATGGACC
ATGAGGAAGCTAGAAGAAAGCACGTTTTCCGGTAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIKFLQVMQKHGYIGEFYIDHRSGK
IVVQLNGRLNKCGLVISPRFNVKIGDIEKWANLLPARQFGYVILTTSAGIMDHEEARRKH
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGGCTGAGAATTTTACCAAGGCCCTAGGTGATATTAGATTCCAC
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAATATCATGTATC
TCACCCCTCTTCTTGGTATTAGTAAAGAGACGCCCTGATCTTGTAAACAGTGGTGAAGATTGT
ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAGGCAAGGCAGAGGCGATGTACATAAA
ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAC
TACTATAAACGTTTGTGTTTGTTCCTTACGCACAATATCCTTGCCCTAGAAATCGTTTGTGA
AATTTAAATTTTATTACCATTTATTTGATTTCGCCTTCAGAAAAATATGGAAGAGTGCAT
ATTTAAAAAGGACTATTTTCAGCATATAGTAAAGTCAGGTTATTTGTTTATTTGCGATAT
CAGAGTAACTTAACTAATACTATGCAGGGCACTTTTAAAAAGGTTTACCATCCACGCTTA
CGCGGATGTCTTCTTGGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG
AATACCAGATCAAACAACCTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAGCA
CCAAATACTCCAGGGGAACCTCTTTGAGGGATATGTTTGATTTCGGAAAAGACAAACCACA
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAACTCTGGACTTTATGACGTGCAAGTCTTCC
AAAAGACAAAGGGGAAATTGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT
TGTTTTTTTCTCATTTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG
ATATGTTAAGGGGTAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
TGAGTAGTTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG
AAGCTGATGCGCGTTTAAAGTTTAAATGACAGTAACGTCCAATCATCGAGGTCAATCTTG
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTT
CATCTTGGCGCCAGCCATTTTATTTTCAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA
GGGAAGAGCTCTTTTGCAATAATGTCTTTTCTGGATACGTCTTTCTTGTGGACCAGCAGT
TAAAAATTAGGTGGGCAGCTTGCGGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA
AGTTTGCCAAACGTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFKRFYHPTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTKGKLFAPVSYWKEDKALFFPHLI
GTAMDGTTKQONIEDMLRGKTSIVRLFSTASGDKLSSSYFQGI VDDNKKTDYLTADARLS
LNDSNVQIIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFEC SRGQWPFSVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAAGTTATACCAGAACCATCCTTCCCAAGGCCTTTTCCCGCAACATATCC
CATACTCGAAAGTAACCTTCGCACCAATACCATATGTCTTCGTAAATTTTGAGATCGTTGG
GGCATTGCCGCTACTAGTTTTCAAGGCATCATTAGTGATGTATGTCATGTCACTATTCATGCT
TGAATTATTATCTTCTCATCGCTATAATTATAGGAATCGATTCTTCTTTTTTTGAAAAA
GAACTTTTTATCTGTGTTGGAGTCCGAATCCTCCATGTTTTGGCGTACTGAAGGCTTAAG
TTCTTCGACCTCTCTCGGTTGTACTATTTCGAAATTTTGGATTTTTGTTATTGTTTTGAC
ATAATGTAAATACTAGATGCGCGCTCAAGGCCTCAGTATTAAAAATTGCAAGATATCCC
TAACTTGATAAATTATTTGAAAGTCGCATAACGTACGATAAAATTCGATACTGCGAGGATAT
TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA
GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA
TTAAGAAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAAACTCAATTTTCTAATAGTTG
GCTTGAGACAGCAAGGAAAGTTCTTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC
TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAAATGAGCA
TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG
TTAACTTATTGAATGACAAACTGAAAGAAGTGCCAGTAATTGAGCGTCAAATTGAAAACA
TTAAGCTTCAATACGAAAATATGGTCAGAAAAGTTAACAAGAAGTGAATGATACCAAGT
TGACGGACGTAACCTCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA
ATGTTGTCAGAGCAGTTTAGCAGGGAACCTAACGGACCTTGAAAAAGATTTAGCAGAGATAA
TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA
ACGATGAACGTTGAGGAGCTGTTTAAAGTGGTACAAAGGCGACGACAAAGAACATACAAACA
TTTTCAAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTTCTTAACTTGGGTC

AATTTTTGCAGGCAAAAATAAAGGAAAAGACAGAACTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAATTCCTGTACACAAGATATTCAAACAACTAAGGAACTTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAACATATATTGAAAGATTGTGAAAAGCAGTTGCAGAAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAAATTTATAGCGGAAAATGGAACCTATCTTCCTG
AGACAATCTGGCCCGGTAAAATTGACGATTTTTCTTCCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)

MNEADVTKFVNNARKTLTDAQLLCSSANLRVIDIKKKLSSWQLSISKLNFLIVGLRQOGK
FLYTILKEGIGTKLIQKQWNAVLVVLVDENMYQYEITSKVQRLDGIYNELSIKDDDT
DPSKLGDIYSRDNVNLLNDKLKEVPVIERQIENIKLQYENMVRKVNKELIDTKLSDVTQK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLLLQDKKIDNDEREEL
FKVVQGGDKELYNIFKTLHEVIDDVDKTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLDISFKNSCTQDIQTTELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCQKQLQNLDAQDQEERQNFIAENGTYLPETIWPBKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
949-1342 (SEQ ID NO 207)

ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTTCAG
AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAACTGTAAAATCCGTACACACTACTG
AATTTTACATCCATACATTTTTTTTGAATTTTCATGTTTTTTTGAATAATTGAAAAGGGC
TAAATTATCCGTCGGGGTGTCCTCCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG
GGCCATCCAAGCTCATCTTCCAGAGATTGCGCTTTCAGAGGCAAAGAAGTTCGTCTCCGC
AGGCTCTTGTTCGGGAGGAGAGAAATCTTGCCTGCGGAAAGTGGTTGATGCCTGGGCTA
TGGTAATTCTGACACCTTTGCTATCCTAAGTGAAGGTCCTTAGTAATAACAATATCA
GGTACTTTAACATTGTTAAAGATATACTATTAGTGAAAAACCGATCTTACGAAAAGCCAA
TAGAGCAGAAAGTGGTAAAGATGTCTTTAGTTGTACAAGAACAAGGTTCTTCCAACACA
TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTCACATTACATGG
GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCACCTCCGATGGAATAATAACG
TCACGGGTTACCAAATACGAGGCCGAATTAACCTACGCTACTATAAAAATTATCACTAG
ATTTTAAAGTAATACACAGTTTATTGGAATAACAATATATGACTCAATGCGAATTTAAA
AATTTTCAGTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTTCGTACGCCA
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCCTAGCAGTGGTGTGAAATAA
ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTAACAATCAGTTTGTGTAACAC
CAATGTGCGATGGTAACATTAATAATTGTTTACGCTTTGACCACTATTAAGGGTGTGTCG
TCGTTACTCCAACCTGGTCTGTAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA
ATTGACCCAAGAAGAATTGGAAGAATTGTCCAAATCATGCAAACCCAACTCATTACAA
GATCCCAGCTGGTTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC
TTTGGCTAACAACGTCGAATCCAAAGTTGAGAGATGACTTGGAAGAAGATTAAAGAAGATCAG
AGCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)

MSLVVQEQQSFQHILRLNNTVDGNIKIVYALTTIKGVGRRYSNLVCKKADVLDLHKRAGE
LTQEELERIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLRLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)

TATATTATTTTTTCCCTTCTGGGTTCTTTTCTTCCCTTTTCTTGTTTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTTGTACATCCATACACCATACA
CCATACACCATAGCACCAGTACACTATATTTTTATGAATTTTACTAAGAATTATTCCTGC
AGGAGCTCCACTGAAAAAAAAGAGCAGCATGGATGTCCGGTAGAAGTGCTACTGAGTAA
ATGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGCCGGTGTGAAGCCGCTC
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATTGCCACGCTGAACGTAACACAGTTTCA
CAATACCAGTGTCTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA
TGTGAGTGGTAGCAGATTTGAACTTAGTTAGTTGTATTGCGCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGGCTGTTGGTAAGAATAAGAGACTATCCAGAGGTAAGA
AGGGTTTGAAGAAGAAGGTGCTTGACCCATTTACCAGAAAGGAATGGTTTCGATATTAAAG

CCCCATCCACTTTTGA AAACAGAAATGTTGGTAAGACTTTAGTTAAACAAGTCCACTGGTT
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTGCGAAGTTTGTGGCTGACTTGC
AAGGTTCTGAAGACCATTTCTTTCAGAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGGTA
AGAAGTTGTTGACCAACTTCCACGGTATGGACTTCACTACCGACAAATTGAGATCAATGG
TCAGAAAATGGCAAACTTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAATCTTTGCTATTGCCCTTACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT
CTTACGCTCAATCTTCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA
GAGAAGTTCAAACCTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAGTTATCA
ACAAGGAAATCGAAAATGCTACCAAGGACATCTTCCCACTACAAAACATCCACGTTAGAA
AGGTTAAGTTATTGAAACAACCAAGTTTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAAGGGTAAGAAGGTTTCTGGTTTCAAGGATGAAGTCTTGAAA
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKKGLKKVVDPFTRKEWFDIKAPSTFENRNVGKTLVKNSTGLKNASDA
LKGRVVEVCLADLQGSSEHFRKVKLRVDEVQGNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVI SEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIFPLQNIHVRVKVLLKQPKFDVGALMALHGECSGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT
CTTTATTTCCACTTCTTTACAAGCTTTCTGCCTTTCTCTATGACGCTTTCCCAAAACAC
TACCTCTTGACACGACTTGTGTTTTTCGTTTTCTCTAAGAAATATCACTATTTTCACTTT
TTTCACTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG
GGGAAGAATAAGGGATCTTTGGAAGTGAAGGAAAATAAGGGAGAGGGAGGAAACAAGGAG
GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCTTAGCATG
ATTAGATTACCGGAGTTTAGAAGAGGATCTGCAATAGAAGAGGAGACAACACAAAAGAA
CTGTTAATTAAGAGAAGAAGATGAAGCAATTCAAGTTGGTTAATGCGGTTTCCGCATCAT
TTGTGCTTATTGGCTTAGTGTTGGCCAATTCAGATTCAGTGTTCGACAAGTGGACGCAGG
AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAGAGTACGCTACAGACT
CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC
CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTACGCTGAGCAACAGTAACCCCGGATGGT
TTGGTTATACTGGTTCTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CAGACAGTCTACGTAACCTTCTTGAAGAAAACGGCGTGGATGTTGACGACGCTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA
AGTCGTCGGGATACTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTGC
AAAACCTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC
TAGTTCAAGAACTCAAGGAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC
TGGGTTTGCTAGAAAGCTTGGATTGGCTTACCAACAAATATTAGACACATCGGGACAAA
TAAAAGACACTGTATTTGACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC
ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA
AAGAAAATTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG
AGTCTTCTCCATTTTGGACCAAGACCCAGAATACGTTGGTTCCGTTTGGGACTCTTCTA
AAAATTTCTTCACAAATTTGTACTCCAAGTTTCAAGGTAAGACTGACAATGTGATCAATG
ATACTTTTTTGGTTGGCCTAGACTCTTGGCCAAAGGACAAATTGAAAATGTTTTTAGATG
CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA
AATCCAGAAACGAAAACTCAAGATCTGCCAAAAGACTACCAAAAATACTTTGACAACA
GTAAGTGGTCTTTGGATGACATAAAGGGTTGGTTTGCTGACAAAAGGACGACTTCCAAG
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGACAAGGTTTCCAAAAACACAAATG
ATGCTAAGGACCAATCGCTAAGACCTGGTCAATACCTTTTCAGAGCTGGTCTCAAGAAG
ACCTATTGCAGTACCTAAAATCATTCGGTGTTCGGGTTAAACAGACTTCTACGAAGGACG
ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTCCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAAACTGGTCGAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKPWQVWSSDSSSVSNPNPGWFGYTGSSDHPVSDWLFDTWSTD SLRNF

LKKNQVDVDDAKASKDSLVTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNLNDN
GIDYDKAVQSKDELVQKVKENIYRTSEKAEQORLGLLESLLDLAHQQIILDTSGQIKDTVFD
KWSSDQLTNWLESHKVNIDKNMAKKHDYLVMAKENSANLKDDIYWYLDYMKRESSPFLT
KTPEYVGSVWDSSKNFLTNLYSKFRGKTDNVINDTFLVGLDSWPKDKLKMFLDARGIKYS
MLSTEHQLRELVKRSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFGVFPVKQTSTKDDLINLAK
QNTQWLFQTVKEPAYKRYLHNVKNWSKSLGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTTCTTATCTATCTATTGAGTAATGCTTACTTTTCATATTTTCAATGAAC
AATAGGATAGTAGGAGAATTGATATATTTACTGCGTATCAGAGAAAAGGTCTACTGACA
TTTTATGGCAAATGTATTCTACACAAATACCAAGATAATACCAAGACAATGGTACAAGACATA
CACAAAGAGAAGACTGTTCTAATTAAACAAATAATATTGAGCTACCTGCTAAGTATGTCC
TTTTCCCTTTGTCCTTTGGTTTCTCTTATAGAAGACCCTGGAAATTTTTCGCATTTTCC
GGCTTTGGGCGTTAGTAAGAACAAAAAGAAAAGAAGAGAACAAAAAAGAAACGATACGGA
GTACGTGTCATAAAAACCTTGTTCAATCATCCTTGAAGCTAAGTATAAAGAGCTTGAAAAG
GTTTACCACTTAAACTGGTTATACTATTTCAAGAGTGTAACATTTTATTGCATATACCA
CAGTAACGTGCAGGTAAAACATGAGATTAAGAACCGCCATTGCCACACTGTGCCTCACGG
CTTTACCTGTCACACTTCAAACAATAGCTACATCGCCACCGACCAACACAAAATGCCT
TTAATGACACTCACTTTTGTAAAGGTCGACAGCAATGATCAGCTTAGTCCCAGTTGTAACG
TAACATTCATGAATTAATGCCATAAATGAAAACATTAGAGATGATCTTTTCGGCGTTAT
TAAAATCTGATTTCTTCAAATACTTTTCGGCTGGATTTATACAAGCAATGTTTCAATTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG
ATACACTGCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAATGA
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACCAAGTA
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA
AAAACGCCGTTCTGATTGATTTAACAGCAAAATCCGGAACGATTTACAGGTTATGGTGGA
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACCTGTTTACAAATGGCGAAA
CTGGTGAATCATTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCTCTA
TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAACCTGGTAAATGGGAGCCCAATC
TGGATTTGTTTATGGCAAGAATCGGGAACCTTCTGATAGAGTGACAAACATGTATTTCA
ATTATGCTGTTGTAGCTAAGGCTCTCTGGAAAATTCACCATATTTACCAGAATTTTCAT
TCTGTGATCTGATCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCAGCTGG
ACACAAAATTTTAAACGAAGACTTAGTTTTTGGCCAACGACCTAAGTTTGACTTTGAAGG
ACGAATTCAGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGGCGATA
GATGTAGATTGTGGGGCAAATTCAACTACCGGTTACGCAACTGCCTTGAAAATTTTGT
TTGAAATCAACGACGCTGATGAATTCACCAACAACATATTGTTGGTAAGTTAACCAAT
ATGAGTTGATTGCACTATTACAGACTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA
ACATGTTTCGAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT
TCTTCCAAAATAAATTCTTCAACATTTTGAAGGAGGCAGGCAAATCGATTTCGTTACACCA
TAGAGAACATCAATTCCACTAAAGAAGGAAAGAAAAGACTAACAATTCATCAATCACATG
TATTTGATGATTTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTTAACGGTACAG
TAAATAAATGGAAGAAAGCTTGAATACTGAAGTTAACAACGTTTTAGAACGATTCAGAT
TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG
TATACAAAATTTTGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNSYIATDQTQNAFNDTHFCKVDRNDHVSPPSCNVTFNELN
AINENIRDDLSALLKSDFFKYFRLDLYKQCSFWDANDGLCLNRACSVDVVEDWDTLPEYW
QPEILGSFNNDTMKEADDSDECKFLDQLCQTSKKPVDIEDTINYCDVNDNFNGKNAVLID
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNKTKGKWEPNLDFMARIGNFPDRVTNMYFNAYVAKALWKIOPYLPEFSFCDLVNK
EIKNKMNDNVISQLDTKIFNEDLVFANDLSLTLKDEFRRSRFKNVTKIMDCVQCDCRCLWGK
IQTTGYATALKILFEINDADEFKQHIVGKLTKEYELIALLOTFGRLSESIESVNMFEKMY
GKRLNGSENRLSSFFQNNFFNILEAGKSIRYTIENINSTKEGKKKTNNSSQSHVFDLKM
PKAEIVPRPSNGTVNKKWKKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATTT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAATAGCGTCTCTGATAGCCATGGGT
GAAGGTCTTCCTCTAGTTCTCACCTTAATTAGCATTCGGTGAGAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCCATTAATATTATCATC
TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAAACAAGGCGCCTCATCG
CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT
CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT
AAACTCTGGCGTTTAGCGTACGAAGGAGATTATCCTAAAAGGAACTTCCCTAGTAATAGT
GTAATTTGGAAGGGCATAGCATGTCGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA
TATTCATTTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGTTT
TTAATGCTAAGCTAGAGTTTCCTAAAGACTATCCGTTATCTCCACCTAACTTACTTTCA
CACCCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCACTGTAC
ACTCCCCTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCGCCAGTGC
AAAGTGTAGAAAAAATCTATTAAAGTGTTATGAGCATGTTGAGTGAGCCCAATATCGAAA
GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPDPYADGVFNAKLEF
PKDYPLSPPKLFTFPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG
TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTAACCAGAAGTAC
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG
AGTAAACACTTCTACCAGTATTTCTTTACGGTTCGGATCAAAACCATCACTCATTCGGTC
ATTCTTACCGTACGATAAACCAAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC
ATCCGTAATAGTTTTTTTTTCTATTTTGGACTTTTGTAAGGAAAGGATTAGGGATACGTTG
CTCATAAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAATGAAATAGTATCAAT
ATACCGAAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
TATTCAGAACGCTAAGAATAATGAAAGCAACCATTTCAAAGAGTAACATCTGTATTTGGAG
TTCCCCGAGCATCTGTATTCGTGCCAAGAATCAGCACACCATTTATTTTGCATAATTATA
TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAATTCCACAATGGCCGCGTATCCAAAT
CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAC
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCCTCTTTAC
ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG
TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA
AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC
ATTTTGGTAAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
GGGTTATAAAAACCGGATCAATCGTTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN
KEEELLVSQRKKRPISPHLTVYEPMSWYLSLHRISGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACCTATCGTGAACCTCGCTGCAACAACCTGAGAGGGCAAGGATATACATA
AAAATAGCCTACAAATTCTGAACTCTGTAAAGGAAGCCTCATAAATAAAGGTAGATAGTA
AAGTATACAAGAGAAGAATCCCAAGATGTCAGCTGTCCCAAGTGTTCAAGTATGTTTTCA
GTTCTGCAGAATGATGTTTGATAGTATGCATAATGGAGTGAGATCAAGAGAAAAAATG
AATATGTCAGCCAACCAAGTTCAGTAGGCAGTAAATGAGTACGCATAGTGATTTATC
CAAAGGAAAGAATTGTTATTTTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTTGG
GGAGAGTATTTTGACAAGATTGGTTAAACTACTACGGTCAGTTCCGTAACCAAGTACGATT
GTACACATAAGGAAACAACCTGTAAAGATAACAATAAGGGCTTCCAATGCCATTGTAAGA

TATCATATTCTTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTAAAAATGGCAAGCGCTACATTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCTCATTTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCTCTCGTAACATAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGGTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGGTTAGTTG
CTTACCATCAAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACCT
CTTACGACAGAACCTTGTTGATTGCTGATTCTAGAAGACCAGAACCAAAGAAATTCGGTG
GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATTTCTTACACCTCGTACTGTATTTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTCGTAACTCCCATTTACCAATCACTATGAGCCGTCCACG
TTTCCAAAAAACCTAAACATATGATGCAAACCTCCAATGAGACTCAACGTAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG
AACATCTGAAGTGGATAGATTAATCGTACAGTAATCGTACAGTACTATGCTTACTGATG
TCGGGAATCTCAGGGGCGACCGCCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAT
AAAACCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTCAGA
GCTCAAAGGAAAAATTCAGGGCGATGCAAAGGTAGTGAGTGACGCTTTTAAGAAAATGG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAAAAACACAACCTATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)

MNTDQQKVSEIFQSSKEKLQGDQVVDFAFKKMASQDKDGKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)

GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT
TCGATGTGGCAGTGTACGAGAGCCATTCTGTATCGTTTCGACAAAGTTTGCATGACTTCAT
GTTGTTTCGTAGCAGTATTCTGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTG
TTCTTGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT
TGTTTCGCGATGTGCTTTTGGATAGCCTGGGAATACGAAATCTTTGTCTTCCGTAAAGTCG
CCGTTTCTTTAACCATTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCAACATTA
CCGCCTTGTTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC
CTTTCCTCTAGCCAATGACTCCAAGCTGGCTGATAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATACCAATGATCACCCAGCCTGCTAAGTGCCCTCTATTGATCCGTA
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTTATATGTGCATTGCAAAAGCATAAACA
AATCCTGGCAGCCGAAGCCGGGCAATCCACTTCGAAACGCACGGCTGAACTATATAAATA
TAAAGGACATGTGGAGAGAAGCTTCTCTTCCCTTCACATTTTCGATTTTCATGATCTAAAGT
GGTTCTTTTACAATAGAAGAGCACCAACACGAAATATGGCTGTGCGTGGTAATAACTGGA
GCATGTGGCTGCGAATGTACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA
CGCTGATCAGTTTTCAGCCATGGGAATTTTCCCAACCAATATAATCGCAATATTTTTGTCA
CTTGGTGGAAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAAACGG
TATCTCCTCTCACGAGGAGAGGAATCGCAAGGTTTGACCATTTTCAGACCTGTTCCCAATG
TCAGTAAATTTGCTTCTTTTCCAGAGTGGCCAAAGGAGCCCCAAGGGGCCCTTTTACCA
ACTGGAATATGACTACATCAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAATTTACCCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTCAACT
CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT
CTAATGTTACCTCTAAACAGGATCACGTCCAACAGTTGCCCTTAAGAAGTTATCTCAAA
AGGATATCAATTTTCATTCGTAATTTAGAATATTTAAGATAATGAAGACCCAGAATGAAG
TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTCCCTATATTGAATTTACCA

TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTGTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAATAATCAATATACA
GTAGTGTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTCGAATACATTTTCCAAACTCAACTGTGGTGGAACAGAAAACTAATTGCAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTTAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)

MITQPAKCPLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLPSHFADFHLKWEFFHNRRAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDRTLISLSH
GNFSHQYNRNIFVTWWKSLFEASTAFRRASGLTVSPLTRRGIAFRDHFDPVNVSKFASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLRCFFNSLGGNLQ
CSHSNSCKAYQNASNVTSKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDETS
YYMEKPGSYIEFTISEFNVNGTFSAPLSFLDPSLLADLDEMIRNYKYLKSIYSSVDMIL
QNYGSLPITFHRNKIRIHFPNSTVVEKLIAGLNIAITGVIIYADTSPDISLEGTNLNLV
NVDNSGVSWSFVKEPSFSPRSASFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)

ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCACTTATTTTTTTTTGGATTTAGATGTGAGACATACTAAAAAAGTTGCTATCAAGCC
TATAATTTGGCTACGTTGTCCTCCGGTGTTTTTCAATTGATTTAAGTTACAACACTCAA
TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCCTAGAGTTCGC
AGATTTATTTTGTCAATTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTAAAGTTGCGTCTCAAAAT
AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAAGGTATACGTCT
TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACCTGAAACCAAGAAAACACAG
ATCATAACTAACC GTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAAATTCACCAAT
ACTTGTTTCAAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT
GGATAGCAAAGATGATAAATGAAAATACAATTAAATTGAACTTGAATATCATTTAAAGTG
GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCAATGAATCCG
AAAGAAAAGTGCAACCTAAGCAGAATGCCCTTTTCACGCGTCCATTTTATAATGTTT
GAACTTTTGAGTCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT
TTACAGTTTCCGGAGTTTCCGTATTATTGCAAAAGGACCACAAACAATTGAAATCATGAT
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT
AGAAGGTGTTGTCGTCGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC
CAAGAACCTTGATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC
TCAATCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG
AGAATACTTGAACTTGCTGAACACATTTGTCCCAGGTACCTACATTCAAGAAAGAAACCC
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)

MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLP EHVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)

CCCTTCGCTAAATCATTAAGAGGTCATTCATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTTCAGATAATTGTCGTCGC
ACAAGACTGCCCCCTCCCGTCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCCTG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTCGTTCTTCTTATTTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCCCTTCG
ATTTTGCATAATGATCTTCAATTCTACAATAAAATCAAGTAGATACAGGAAAATATTTCC
ATAAATTATAGTGTAATCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCACTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTGCAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAAATAGTTG
ATGATTCTGTGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTTGCCACCA

TAGATAACAATTTAATGGATTCCGATGCCACGTCACATAATCAAGATCATTGGCATTTCAG
ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG
AACATATCGGCTCTGTTTCATCAACTAATAATAATAGTAACAATGCCCTAATCAACCACA
ACCTCTGTGCATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTTGGTAGCTTCTAACCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG
CCGTCATCTCCAATAATATGCCCTACAAGTAACATTGCCCTTTATCAAAACAGCGAGATCGG
CGAATATTCATGGTCCATCATCAACTTCCGCATCTAAAGCGTTCAGAAAGGCTTCGGCCT
TCTCCAATAACACGGCACCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC
CTCTTTTACCTCTACCTTCACTATCACAAACAAAATAAGCCAAAATAATAGAGAGGCCCA
CAATGCACGTCACATAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA
AGCGAAGAATGACTCCCGGAATTCAACCACACACGATAATGGTCCAGTAGCAAATGATG
GGCTGCGTATACCGAATCACTCGAACGCAGATGATAATGAAAATAACAACAAAATGAAGA
AGAATAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAAATATGCA
CTACATCTACTAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACTCAGG
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACATAATAACAAGAAGAAAA
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA
TCAAGAATTTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAATAATGCAATAAATGACG
ACTCACATGAGAGTAATTCAGAAAAACCAAAAGGCGGATTTTTTCGCTGCAAGGCTGG
CTACAGCTGTAGGTGAAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG
CAGCTAATTCGACTAAAAACCTAATATTTCTGACTCCTCCAGCCAGCAGCAGCAGC
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAAGATAA
GCGCCCCATTGCTAAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA
TTAGCACTGGTGCCATATTGAATAACACAATCGCGACTATAAGCACAAATCCGAACCTTGA
ATTCTAATGTGATGCAGAACATAACAATCTGATGTGCGGACACAATCACCTGGACGAGT
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG
TACAATCGGTAGATTTCGTATACCTCTGACAAACCCAGACAGCAATGTTATTGCCAAGTCCG
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTTCATCCA
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAATTCGCAGGAATTGG
AACCAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACATTCCT
CTGCTAATAGAAATTTCTAATTATGGTGACAACAAAAGGCCTCTTAGAACAACAGTGTCAA
AGATATTTGATTCAAACCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG
TGAAAAAGGATGAATTTTATAACAGCAGGAAACCAATAAGTTTCCCCATGGTTTAACTTTT
ATGGTGATAACAATGTTATTGAAGAGGAAAAATAATGGTGACTCGTCTAATGTAAATCGAC
CGAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG
ATATTCACCTCATGTTTATTATTAATCATAAGAACGATTTAGAAACAAAACCGCTAATAT
CCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCCAATGCTACTTTCAACA
GTTACTATGGCTCAGCATCCAACACGCACGAACCTCCATTACATGGAAGGATGCCTTCAA
GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT
TGAATGAATATACCCCTTAAGAATGAAACGCTGACAGTAATGGAACAGGAACGGAAAA
ATAGCATAATGAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA
TCAATAATAACGATATTGTTGGTTACTCACCGCACAACTTTTACTCAAGGAAGTCCCCAT
TTGTGAAAGTAAAGAATTTTCTTTATCTTGCATTTGTTATATCATCACTATTGATGACAG
GATTCATCTCTGGGATTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
TGATGGATAATGTGATTTCAAGTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT
TTAATCCAGGATTCTTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTCAGAAAA
GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA
TTTTACAAATAACGACAAATCTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAACTAGAGACACCATTAAGT
TCCAGGGCGGCGCATTTAATAGGAACCTACGATGTGTGCTAGTCTCGAGTGTCAAGCTTTTAA
GTCCTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG
ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAATGCTAGAG
ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTCAATACGCAAAAATCTACGGCTA
TTCAAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANLLLSNNSNVVAPNPSIPSASTSTSPLHREIVDDSVATA
NTTSNVVQHNLPIDNNLMDSDATSHNQDHWHSIDINRAGTSMSTSDIPTDLHLEHIGSVS
STNNNSNNALINHNPLSSHLSNPSSSLRNKKSSLLVASNPAFASDVELSKKKPAVISNNM

PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNTPSTSNNIGSNTPPAPLLPLPS
LSQQNKPKIIERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH
SNADDNENNNKMKKNKNINSKGNERNDTTSKICTTSTKTAPSTAPLGSTDNTQALTASVS
SSNADNHNHNKKTSSNNNGMNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS
EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQOQQOQQPPKQ
QOQQQNHGITSKISAPLLNNNKLLSRLKNSRHISTGAILNNTIATISTNPNLNSVMQN
NNNLMSGHNLDELSSIKQEPHQLOQQOQPPMDVQSVDSYTSNPDNSNVIKSPDKRSSL
VLSKVSPhLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN
YGDNRPLRRTTVSKI FDSNPNGAPLRRYSVGPDPHVNLEDYIEQPHNYPTMQNSVKKDEFY
NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFI PEDNESDENDIHSMFY
YNHKNLLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGRMPRSRNNNDYY
DFMVGNNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNDIV
GYSPHNFYSRKSPFVKVKNFLYLAFVILLSLMTGFI LGFLLATNKELDQDVVVMDNVIS
SSDELIFDITVSAFNPGGFFSISVSQVDLDIFAKSSYLKCDSDNGDCTVMEQERKILQITTN
LSLVEESANNDISGGNIETVLLGTAKLETPLKFQGGAFNRNYDVSVSSVKLLSPGSREA
KHENDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDYELIVRGS MK
YEVPPFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTTGGATTACTGCTCCTCTTTTAAGAAGACAAGTG
TGTGATATCGTAGCGGTAGGAACCAATTTTGCAATCGATTACTTACAGCCAAGAAAATC
TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTACACGTTGTGCTTGCCAGGAAC TA
TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTGCATCTGATGT
GTAAACTCATGTGGTGCACCTGGTGTGTTTCCAAGACTGCAC TATTAAGTGGGAATTTTT
TTTTTCTTCTAGTGAATTTTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATTATTTAA
ACGGACGGCAAACATGAAAAAAAATTACCAACCATATTTCTATTTCCCTTTCCCTTTAC
CTATTTCTTTTGAATAGTTTCTTCTCTCTGAAACGACAATAAACCAAACTCTA
GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAACAATTGAAATCCCAG
AAGGTGTTACTGTCAGCATTAAGTCCAGAATCGTCAAGGTTGTCGGTCCAAGAGGTACTT
TGACCAAGAACTTGAAGCATATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTCAACCGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT
TGGTTGACAACATGATCACTGGTGTCAACCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCTAAATTCATTGAAG
TCAGAAACTTTTGGGTGACAAGAAGTACAGAAACGTCCTAGATGAGATGGTGTACTACTA
TCGAATCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG
TTTCCCAAATGCCGCTGACTTGCAACAAATCTGTCTGTTAGAAACAAGGATATCCGTA
AGTTTTTGGATGGTATCTACGTTTCCCAACAGGGTTTCATTGTCTGAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVMNQLIKVAHVHNG
DRKHVAALRTVKSLVDNMITGVTKGYKMYRYVYAHFPINVNIVEKDGAKEIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVNRNKDIRKFLDGIY
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAAATGGAGATC
TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAAC
AGTAATGGAAATGGTAATGATGACACCTCTAATCAGAGAACCGAAGCACTGGGGCGTAAG
ACGAGTAATGGAGGCGGAATATGATTACTAAGTTAAATAAATCAGATACAGTATTTAAAG
TTCTTTCAAAAAAAGATAATGTCATATATTTTACTATCTACGCAGTGAAAAGAGTTCCTTC
TAATGACACACTATTTACTTCCGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
TATCCCGGAAATGCGATGAGATGAAAATGCATGAAGTAGCGTATATATTGATTGCATGAG
GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGTTCCCATAAAT
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT
ACAGAAAAGCGCAAGAATTACAAGATTTCAACTGCAACAAAAACGTCAAATAATTAAAC
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAAGTAGCAGAAGATGAGAGTTTACAAA
AGGATTTTCAAGATATGACCAAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACGATTG
ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC
GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAAACTGCTATTTCCAAATG
CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTAAAAAAT

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGGC
CCAAAAAGATTCCGAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAGAGAGGGAGTAGAGATTGCCGAAGTTGGTCCTAGAT
TTGAGATGAGGTTGTTTGAAGTGGGAACTTTAGAAAATAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQKQRIIKQALAQGKPLPKELAEDESLOKDFRYDQ
SLKESENEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVMVRHDIINAG
NQSEVNPHLIFDNFTTALGKRVVCI LKHLFNAGPKKDSERVITFANRGDFISVRQHVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACCTTTCACACACCTTTCATCAGAGAGAAATGTTG
ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTCTGCATAG
TAGTAGTTACGAAAGGCACAGAAAATAACAAAAAAGTCAATTTTCTACGGT
CTCCATCCGTACCTCTTTAAATCCGTACATTATTTGTTTGGCTTAATTTCAATATTTTCGGA
AAAAGCGAGCGCCCTGGTAAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACCTCAC
CAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTCAGCCTGGCTTTAGGGAAGAA
TGGGCTCACTAGGCGTTTATAATACGCGGAGGGGGAAATACCAAATGCTATTGATTATGG
TTAAATATGTGTTATTTGACTTTGTATATACAAACAGAAGAGAAACCAACACACTAAAG
ACTAGACACATAACTGACCAATGTCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA
GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC
TAAAGGCTGACTTGAGACCATTGCAAAATCAATCTATCAGAGAAGTATGTTAAAAGTTAT
ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGGTCTTTGCAGTAATTTTTT
CAAAAAAGAGTGATTTTGGAGCAGTATCTGTATGAAATTTTCATGTGTTTCGAGAAAAATAG
TAATTTCCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT
CCTTGGTCACTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA
AGGAGAAGAATCACAAACCTTTTTTGTATTGAATGAACCAATTCAGTTACTAACTTTAT
TTCAACGCTGCTTGATTCTTATTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCAGTAG
TCCTTTTTGTCCCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAATTGACCC
GTGAATTGGAAGAAGAAATCCCTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGAACTCT
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA
CTGCTGTTACGACAAGGTTTGGAAAGACATGGTTTTTCCCAACTGAAATTTGTCGGTAAAA
GAGTTAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG
TTCAACAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA
AACAAATTGTTTTTGAATTTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHVI FLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKVLEDMPFTEIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
987-1333 (SEQ ID NO 235)

TTCATCACCAATATAGACTAATGCGTTTTTGGAAACGCCAAACCGCAGTGACAAATAGCAAA
TATGTAGCTGTCATATCGGCATATAATAACAGTTTTTCTACCAAATGCTGTCCTACATTCA
GAGATCTTACATCCTTACATCTAAAGTAAAACCTAGACATTTACTTCGAGTTATACTTTTT
TTTTTATTTATCTATTTTTTCTCTTGGCAGCATTTAACACCTGAATTCGCGCTAACGCCA
GGACTGATCTTCCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGACCTAGGAGAA
GGTTACAGCAGCTGGCCCCGAGAGTGATTGGGTACAGGAAATAGCGCAACCTTCTCTTT
TGCCCCGGAAAGGCGGTTCAATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC
AGATAATAGCACCATTAAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
AACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCCTAATGGTGAATAAAA

TCAGGACCAATAAAGAAAAGCTAATTTGATTTTATTGTCAATGAAATTCATAATCGTC
ATGAATGCATAAACAGACACACCTAGCAACTGTATAATCTGCGCCTAAAAAGGGCGTATA
CACAAAACATAACGATGCGCAATAAAAGTTCAGCAGTCAGCAATGAAACCGAGATATGCA
GCAACAGAGTATCATATGCATGGAGGATCCTTTCTGTTTTCTGATAATATGCTCTGAAA
AAGCTCCAAACAGCACAGTAGCCTATTTGTGAAGCTCAAAAAAGGCTTCTATTTCCCTCG
CTATCTTCAGATTGTGCACTGATATTTCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG
ATAACTGTTATTTCTTTTCAATATGCTAGATTTTGCTTACCACCTTACTGATTTTTCTTA
ATAATAAACTTTTTTACTAACATTAGTACGATGTCTCATCTATTTCTTCTATTTAGTTAA
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACA
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCCTTGTTTGCCCAAGGTAAGAGACGTTA
TGACCGTAAACAATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAA
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT
GACCTTGAAGAGATGCAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGC
TTTGCAATTCTGA

YNL162W, 116 aa (SEQ ID NO 236)

MVRCLIIFFYLNVNPKTRKTYCKGKTCRKHTQHKTQYKAGKASLFAQGKRRYDRKQSGF
GGQTKPVFHHKAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)

GGTCCACGTCAGTTCACACAATAACATTTACGTAGTGTTCACGCGAAGCAGTTACATCT
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC
GTTAGTATTTTTGGCCGCCGTAATTTCTCTTGTTTTTTTTCTTGATTTCACTTCTTTT
CATGTTCCCTTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTGTTCCGT
AACATCCATACCTTTCTGTATAATATTCTTGCTGTAAAGTTTGTTTTTTTATGAAAAA
AACATTTTCTTTTCTTGAGATGAGGCGCCGCGAGCCTTTCTCCCATGGGCAGTGGTAAAT
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTCATACATTTTAAGCAATT
TCTAGTTTGTAGATATTGTTAGATTAGTTTTTGAACATTGTTTTGATAACTGAAAAATAA
ACAGCAAAACAACTACAAAAATGGTCGCTTTAATCTCTAAGAAAAGAAAGCTAGTCGCTG
ACGGTGTCTTCTACGCTGAATTGAACGAATTCCTTACCAGAGAATTAGCTGAAGAAGGTT
ACTCCGGTGTGTAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA
GAACTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACTTTGTTGGTTC
AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAAGAGTTCAAGACC
GTGGTTTGTCCGCTGTGCTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTGG
CTATCAGAAGAGCTGCTTACGGTGTGCTCAGATACGTTATGGAATCTGGTGCTAAGGGTT
GTGAAGTTGTTGTTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTCGCTG
ACGGTTTCTTGATTCACTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC
ACGTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA
AGAGCAGAAGTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTTGAACCAAAAGAAG
AAGAACCAATTCTTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC
AAGCTGAACCAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)

MVALISKRRKLVADGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIIRATRTQDVLG
ENGRRINELTLLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPKASRTGPKALPDAVTIIIEPKEEPI LAPSVKDYRPAEETEAQAEPEVA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)

CTTTGATAAATTAATACGGTAAGATACCGTGTGAACATTATAATAACTGCCACGCTTAT
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
ATCGTGGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGGGTTTTTGAGAGGA
GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTTGAAAGCACCCATTCAAGGAGT
ATGTGTCTGTAATTGAAGTGTTAGCGCGGATTCACCTGTAATAAGAGTGATGATTTGAT
AGCGCCATTCTACATCATATGGCAAATGTTGAAAACTGTACGCGCGAACTAAAAATTTTT
TTTTACATCCCCTAAATGAAAAATTTAAATCGATGCCCATTTCCAAATATGCTATTATCGA
AGGACGGCTCTGACAAGGGCATATGCGTTTAAGATTGATTGTTCAATATTCTATAAAACAGG
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTACAACAAATACCTCAGGAA
CAATAGCTTCTGTACACTCATTTGAACAGATAAATTTGAGGCAATGCTCCACTCAATCAA
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTATTGCTCAAGCACAAAAGCAT

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAAAGAGAATCTGTTGAACAGCGCTTAC
CATTACCTGAAATCCTAAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA
GAATTC AAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT
CCACCGAATCGGGTAAATTTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA
AGCCTATGGCTCATTACCAAAGTATCACCAAGATTAAGTCCATTTTAAACGGCAAGTATA
TTATTACTTCTGGTAACGATTCGAGAGTTATTATATGGCAAACCTGTTGACTTGGTATCAG
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG
ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTATCATGTACTGATACGAAACTCTTCA
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA
AGCAGAAGGCAAACGAAAATGACGTTAGTATTGGTAAGACCCCAGTATTGCTTGCGACAT
TTACAACCTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA
TTGGTACTGCGGAAGGTTGTTTTTCATTGAATTTATTTTATAAACTAAAGGGTAATGATA
TCGTTAATCTGCTACAGTCCGCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC
TAGTGCAACGTAACCTACTAACTGGCGGCGAAAATGAAGATTTGGATGCACTATATGCAA
TGGGCCAACTTGTCTGTGAGAATGTCTTAAATTCAAATGTGTCATGCCTAGAAATATCAA
TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT
ACTCAAAACAAATCATTAGAACTATCCAAACTTTAACTACATCACAGGATTCAGTTGGAG
AAGTGACCAATCTCTTAACCAACCCCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG
GAGAATCCAAAGGCAACAACCTAGTAATAATAATGGTCACAATTTTATGAAGATACCAA
ACTTACAAAGGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC
AGATAGGAGAACCAGAAGCAGAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTA
ATGCCTATTTGGAGCAGGTCAAAACGCAAGAATCGATATTTTACATATCGGTAAGGTGT
CAAGCAATGTAAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG
CCGCTAAAGATGAGGAAATTAAGAACCATAGAAGCATTAACTCATGCCT
ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA
AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTTNTSGTIAVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDEGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWELNSGILLNVKPMHYQSITKIKSILNGKYIITSGNDSRVI IWQTVDLVSASND DPK
PLCILHDHTLPVTD FQVSSSQGKFLSCTDTKLFTVSDATIRCYDLSLIGSKKKQKANEN
DVSIGKTFVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLGNAIVNLLQS
AGVNTVQKGRVFLVQRNSLTGGENEDLDALYAMQGLVCENVLNSNVSCLEISMDGTL LL
IGDTEGKVSIAEIYSKQIIRTIQTLTTSQDSVGEVTNLLTNPYRLERGNLLFEGESK GKQ
PSNNNGHNFMKIPNLQRVIFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDNKIDATSSLD SNAKDEEITELKTNIEALTHAYKELRDM
HEKLYEEHQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTACGTGAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT
TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTTAAGTTTCTTTTACCAATTA
GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTTGTGCGTAATTTTCGTTTCGCTG
ATTACTTTATATAGTGTAGTTTGTCTTGAATGTAATAAAGACTTCTGTTTTATTTTGT
TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTCTCTTTTTCTTTTTTGAATAAA
GAATTTTCTTTAAGGAGTAACTTAAGCATTAGCTGCACATTAAACACTTTTTTTTTTA
CTTCTAACTCACACACTTTTGGAAGAACATTTATTTTTTTCGACCTTCTTTCCCAAATACC
CAGCGCTTTATAATTGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG
TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT
CATCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCCTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACCCCAAACCACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACTCCAAACCACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
TCAACAAAACCAACATGACACTACCCTTATGGTCCTGGTGAAAAGGCCCGTAAGAACA
ATGCCGCCCTGGTCCATCTAATTTCAACTCCATAAAATGTTTGGTGTTACCGCTGGTA
GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKKGEHDFTTTTLTLSSDGLTTTTSTHTTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS
NFNSIKLFGVTAGSAAVAGALLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATTTTTTCATTTTTAATGTCTTAGCTTTTGTATCTTAGATGAA
GTTTTAGTTCTGTATATCACGATCAAGATATCATAAATCATAAATCAATTATCTTCT
GTTTCCCTCTTGAGGCATCAAACGAGTGTGTGACTGATACACACCAACATACTAAGGCA
ACTTTTCTGGCTGCCCAAAGCTGTGGCACGTATGAAACTGCTTTTCGGCTGCATAAAACA
ACCATGTGGAGTTTTACTGTATTTCGCATTTCCGCCCCGCTAGCATTCTTCGTTTCATGCTA
AAAATGAGGCGTGGGCTAATATTTCAGTATTAATAATTCCGGCACCCGCACAGCCCATACC
GAAAAGGGGCTGGCTGTGGGCTTGGCAAAAACTCAATCTGAGCAGTCATTTATAAAG
AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAGCCTTCCAAATATAGATCACTTAAGA
CAATCTAACAAGTGTCCAAAATGTCTGCAAACGAATTCTACTCAAGTGGCCAACAAGGTC
AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGTCTCCAAACAACGGTCAATATGGTG
CCGACAATGGTAACCCCAACGGTGAACGTGGTTATTTTCCACTATTGTAGGTGGCAGTG
CCGGTGCGTACGCTGGATCTAAGGTGTGCAACAACCATCTAAGTTGAGTGGTGTGCTGG
GCGCCATAGGTGGTGCATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC
AACAAGAGCAATACGGCAACTCAAACCTCGGAGGTGCTCCTCAAGGTGGACACAACAACC
ATCACCGTCAGACAATAACAACAATAACGGTGGATTTGGCGGTCCAGGCGGCCCTGGCGG
TCAAGGTTTCGGAAGACAAGGCCCAAGGATTTGGAGGTCTTGGTCCACAAGAGTTTGG
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTCGGCGGCCAGGTGGC
CAAGGATTCGGTGGTCCAAACCCTCAGGAATTCGGGGGCCAAGGTCTGCAAGGATTCAT
GGCGGTTACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQQGQYNQNNQERTGAPNNGQYADNGNPNGERGLFSTIVGGSAGAYAGS
KVSNNHSLSGVLGAIGGAFLANKISDERKEHKQQEQYGNNSNFGGAPQGGHNNHHRQIT
TITVDLAVQAALAVKVSEDKAHKDLEVLVHKSLLVQVAKDSVVQILKNSAARWPRIIRWSK
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTCTTTTTCAAAAAACCGTAATAAATTTGAGGTACACCAACTAAATACAAA
TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACCTCAATA
TAGTAAAGTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT
GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC
CTTTTACAAAGTGGATACAGGTTGCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA
TTGAGAAAACGGTAAACTTTGAAAGTTGCAGATGCAGAATATATATCTGGTTTTGTAGTT
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA
CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTAAATC
AGCTAGTGCATACCAAAAACATGAGTAACCAACACAGCCCTCAGCCATTTTGTTTGGACA
CCAAATTGGTGAAACTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCACAATAAAAAACA
TATTCGCCGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTCTTTCTCAGAAAGA
ATTTACTAGAGTTTTCGCTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG
ACACTATATATATTTTGTGCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA
ATATATTGGAATATGTTTGCCACGGTTTGTTCAGGGAGGACTTGAGGGTTTTTAATA
ATACTTTTACACATATCACGATAACCGCCTACGTATTCTCCAAGAAGACTTTCTCAAT
TGTTCAAAAAAATCAAACTAAGGCTTCTGTACTATGTTTACAGTTGAGGAAATTTTTC
TGACAAACCAAGAAATTTTACCTCAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA
ATAAAGTACAGACAAATGGGCCGCAACGGCACGATTTTCATAGTCACTCTAGAAATAAAC
TGAACAAAACACAAATCACTTTCTCATTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA
GGGAAAAATCAGGCGCCAGCATAAAAATAATACCTATTAGTGATAAAATGACTGCACATG
AAAGGAACCACCTGAATCTGTTCAACAAACAATACTAATTTCCGGGTGACTTATACTCAA
TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPQPFCLDTKLVLLEELQEGKQFNKNIFPEKALYKLALDYSFFRKNLLEFCV
HLDKIKGVIRPNYDTIYILCLLEVLDLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH

DNRLRILQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNQ
PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPE
VQQTILISGDLYSIALAVTSIESALITLTL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGACACAGAAGATGATAAGAG
AGAGAAACAACGAAGAAAGAACAAATGTTGGGGTTCACCCGAGAGATATTGACATACT
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA
TATTTCTTGTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA
TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTCTGGA
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCTGGGTAAACGGAA
TTGTGATAATTAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA
TTAGCAACTATAATAGACTAGTTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT
TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCATAAATTTTGAGCGCCCTATCTT
CGAAATTAGTGGCGAGTACAATATTGCATTTCATCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTTCAGGGAATTCGATCTGCGTTG
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG
GTCAAGAACTCCCCGGTGGTTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG
CAAACATAAATGATGAGAAGAATGTCTGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGACATGAAAGCATCGCCTGGTGACTTGAATTTTCCAGTGATTTCAAAGAAATGA
GAAACATCATAGATTCTAACCCGACTTTATCTTCACAGGACATTGCCAGATTGGAGGATA
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC
ATGAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCGAGTTCA
TTAATGAAAGTTTTCCAAATTTTAAAAGCAAATCATGGCCGCTCTGTCAAATTTGAATG
ATTCTAACACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCCATTTTAAACGAAT
TACCTGTACATCCGAAGATCTTCTATATACTCTACGGTTGTTTTACAAAATGTATATG
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAAGTCCTGGAGTTGATCAGCAAAATTT
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG
AGAATTGGTCGTCAAATCTGCAAGAGTGGGCAAACGAGTTCCAAGAGATGGTCCAGAACA
AAAGTATAGATGAACTACATACAAGAAGCTTTTTTGGACACCCTTTACAACCTGAAGAAAA
TTTTTCAAAGTGACATCACGATCAACAAAGGGTTTTTGAATTGGTTAGCGCAACAATGTA
AAGCCAGGCAATCTAAGTTGGACAATGGGCTCCAAGAGAGAGATACTGAACAAGACTCAT
TTGATAAGAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA
TAAAAAATTTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVASTITLHSSIHVPSGGEIISAEDLKELEISGNSICVDNRCYPK
IFEPHRDWQPIILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSSEDMKAS
PGDYEFSSDFKEMRNIIDSNTPLSSQDIARLEDSFDRIMEFAHDYKHGYKIIITHEFALLA
NLSNENLPLTLRELSTRVITSLRNNPVPVVEFINESFPNFKSKIMAALSNLNSNHRSS
NILIKRYLSILNELPVTSEDLPIYSTVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFDFDTLYNLKKIFKSDIT
INKGFLNWLAAQQCKARQSNLDNGLQERDEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTTGTTTGCATTGATATGACTTGTTTTATGACTAACATATTTAATTT
TTATTTGTTAACCGTAGGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA
TTTTACTGTTTGGCGTTTGTCTATGCCCTGATTTTTGTCACCTATTGCTGGTCTCTTTTATG
TCACACTTGTACCGCTTTTAGTGACATGGGCCATACTGTTATTAGGGCCTCTTGGTGTGA
TACTGGTTCATATTCATGGATTTTACAAACGAATGTCTTGACTGCCTTTGTTTGTAGAA
CACTGGTCCTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTGCAAGACC
AAGATGAATTTCTAAACGAGGTGAAGGTATTGCCTAAACCACAAAAGCCACATAGAAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTAAAGA
TCCCCAGATTATTCAGAATGTTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC
TGTCGCTAATTCCTATTGTAGGACCAATCTTGGCAAATCAACTAATGGCCCCAAAAAGAA
CCTTTACCTATTTGCAGAGGTACTTTTTACTAAAGGGATTTCAGTAAGAAACAGGCCAAAG
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCGGTATGTCTGCCGGTCTACTAG
AGTTAATACCCTTCTTCACAATAGTCACCATATCTAGCAACACTGTTGGTGCAGCTAAAT

GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLPIVGPILANQLMAPKRTFTYLQRYFLLKGFSSKKQAKDFQYEHY
ASFICFGMSAGLLELIPFFTTIVTISSNTVGAAKWCTSLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)

ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCTGGAGGAAT
CATAGGCAAAGAAAGAAAAGAAGTTCATCTTTAAACTACCTTTCAAGCCTTTATTC
GTTCTCGTAAAGGACACACGAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT
AGGTCGCAGGGAATCCTTGAAAGCCAAGAGTTTTTTTTCCGTAATGATCTCCCAAAGCAA
CCATCAACATGTGGTGCAAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAAACAACAAAGTAATGTTCAACTTTCGTA
ACTACGAAAAATAATATATAAGTAGTTAACGAAATTGCAACAATGAGAGCTCTCACATAT
CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAATAATACAAAACACACTCGTACACTC
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
CTTTGGCTTCTGCCCAAACCTCAGGAAGAAATTGACGAATTGAACGTTATTTTGAATGACG
TTAAGTCCAACCTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT
TAAGCAGTCTGCCATCTGGTGTTTTAGACATCGTTTTAGCTTTGGCTTCCGCCACTGATG
ACTCCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGTGTTAGCAAGATGTTGACCA
TGGTTCCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAATCTTA
CCACCGCTGCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT
CCAGTGAAACTACTTCTTCTGCCGTCGCTTCTCCAGTGAAGCTACTTCTTCTGCCGTCG
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGTGCTTCTTCCAGTG
AGGCTACCTCTTCCACCGTCGCTTCTTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT
CCTCTGCTGTTTCTTCCAGCTGTTGCTTCTTCCACCAAGCCTCCGCCATTTCTCAAATCA
GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAACTGAAAACGGTGCTGCCA
AGGCTGTCATCGGTATGGGTGCTGGTGTCATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)

MAYIKIALLAIAALASAQTQEEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLP
VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV
ASSTKAASSTKASSAVSSAVASSTKASAI SQISDGQVQATSTVSEQTENGAAKAVIGMG
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)

CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA
CAAGCATCAGTTTTTTCATCGCAAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC
TCAATTAATAACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTGTCTTAATT
ACTGCTGAATACGCCCTTCTAGAAGACCGTTCTGTTTCAGCCGCTCGCCCCCTTTTCAAAGC
TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTTTGTGAATGGCAATCTACCATTTATAG
TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTTCATGTCTCGTTACCA
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAATAATAA
GGACTCCTCATTAATAAAGGCTTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG
CAAGTCAACCTTAAATTATTATGATTTCTGTTTGGCCACAAAATGACTTGCAAAAATGCT
ACAGAAGCCTCACATTCGATGTTCCAGGACAACAATTCGAAGAGAGAAATGAACAAAACC
TTAAAAAACGGGCCAAAAAGAAAGGCAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC
CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTTCGCCAA
ATTTGCAATATTATTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG
AGAACAAATCTGAATCCAGTAGTTTTCCAATGAGATCCTCAAAGTTGTTGGAAAAGAATT
CTGACATCAAAAAATATTTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC
CAAGCACGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAGAAGAACTGGA
TAAAGTTATGGCGCCAAAGAAAACCTACAAATAAATGAAAGGCTGAATGACAAAAAAT
GGTTTACTTACCCAGAATCTTCTCTGAAGAGCGTATTAAACCGTTATATAGAGGAG
ATGATAGTGACCATGTACAAAAGAACAAAAAGAAAGCATAAAATACTTCAACAAAAGG
TCGGATATCCCAATAACCCTAAGACAATAGTTTGTACATTAAACGGAAAAAACATACGT
GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA
TAACTACACTGCCAAAATGATTTCTAACAGGAAAAAATGCAAAAGATGATACAGAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTTGATTATA
TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAATAATTGTAG
GCAAAATTAAAAAAGTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTC
TTGCTACTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAATCCAAAAAGCTGA
CAGATGTCTTTCTGTTAGTTATCCGATTCCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTCTGTTCAACTGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAATCATA
TGAAGCACGAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA
TATCAGATATTTCTTCACATATTTCCGTAGATTCGTACGCCGAAGATTTCAAAAGGGCAAG
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCGGTC
TCGCCCAGCATTCAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAACTTTTGTGTTGAAGAAAATTGATATCATAATTAGAG
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA
GTCACGGTGACCAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTCGAAAAACA
CAAAGTTTAGAAAAATCTTTAATACCATATTCTTCTCAGAGGAACAAAATACCACAACAA
CTATTAACTCAGTAGCTCGCCTACGTCCCAATCAAGTTTGCAACCTCTGTAAACACAA
AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT
CCTTCGACAAAGAAAATTCCTTTGATCCATCTGATAAAAGCAGTAGTGTTGATAATAGCA
TTCTTTTGAGGAAAGTTAAAAGTGCCGGTGCGTTAAGAAAAGTCAAACTAATGACTCCT
CAAGTAGTGACGGGTCAAAGAAAAGCTCGTCTAGTTTTAGTACTGTGAACACCTTCACTG
GGGGTGGAGTTGGGATTTTAAAGGTGTTTAAAAGTGGAAGTTCCTCTGGAATAAATCAT
CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTTTGAAGTGATGATCGTAACGACAAGA
AAAAGAAGAAGAAAAAAGAAGAAATCATTGTTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQQFEERNEQNKKRAKKKGSFQPSVAFDTPVSTAGYS
SIDDSREGFKGVFPVNYTMEECYDDETDSPNLQYYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLEKNSDIKKYFLVSKNGKIVRRDYPSTPVIIVNETLMINRFEKNWIKLWRQR
KLQINERLNDKKKWFTYPELIFSEERIKPLYRGDDSAFCTKEQKRKHILQOKVGYPNP
KTIVCHINGKKHTWVALDWTVYKFARNLDHIVVITTLPKMISNRKKTAKDDTWEAPGYQK
EVIDQKLNDIFDYILQLVKVVKISVKITLEIIVGKIKKSLVDVINVHTPDFLVLATLKHE
RNENLITYKSKKLTDVFPVSYPIPTFVVPVSKRMYSFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKKNTISDISSHISVDSYAEDFKRQGYIKKQFNTSNDSPRKLTLGLAQHSRR
KITGDIEKLQDDEKDRRECTKEKLLLKKIDIIRESLKSSLAIETLPKKNVSQSSHGDIQIS
SFKNALIGNGSKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFDPSDKSSSVDNSIPLRKVKSAGALRKVKNTNDSSSSAGSK
KSSSSFSTVNTFTGGGVGIFKVFKSGSSSGNKSSSRNSSSGDVFESEDRNDKKKKKKKK
KKSLLFLFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGTCATAAGTTCCTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACCTACAAACCCGCAAGAAAATAAAAAATTTCCGCAAATTTAACGAAGACAGCGTGG
TTAAATTTGCTTGTTCGGACAATATTCTATGTCTGGCAACTTCTGATGATACTTTCAAGA
CAAACGCCGCAATTGACCAAACCTATTGAACTAAACGCAAGTTCAATATACATAAATATTG
ACTATGAGAACTGATATCTTCGTGAAGATTCGTGTAGTATGATAGAACATTCCAGAAAAA
AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAAATCA
CATACATAGATTAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA
TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAATTCCTCACTGTAGCTACTAAA
ACAACCTATACGCAAGAAAGATGTCATTGACAGCCGATGAATACAAACAACAAGGTAACG
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG
TTTCTGAAACTCCAAACCATGTTTTATATTCTAACAGGTCCGCCTGTTTACTTCTTTAA
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAAATCAATCCATCTTGGT
CTAAGGGTTATAATAGACTCGGTGCCGCCCACTTAGGTCTTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC
AGTTGPTTGCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCCAAAAACTAGCGAAA
TGATGAAGGACCTCAATTAGTGGCTAAACTGATTGGGTACAAACAAAATCCGCAAGCTA
TTGGCCPAGATCTGTTTACTGATCCAAGATTAAATGACCATCATGGCTACATTGATGGGG
TTGATTTAAACATGGATGATATAAAACCAATCAAACCTCCATGCCAAAGGAACCGGAACCA
GTAAAGCACTGAACAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG
AAAATTCCTCTAAAGCACCACAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG

ATGAAGATGACTCTAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTTACA
AGGCACGTCAATTTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGGAAGTGCATAAAG
ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCCAATACGAGACAG
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG
TCATTTCCAAATCATTGCGCGTATTGGTAATGCCTATCACAATTTGGGTGACTTGAAGA
AAACTATAGAATACTACCAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCCTG
AAAAGGCCGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT
CTAATAGAGCTGCTGCAC TAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA
ACAAAGCCATTGAAAAAGATCCAAATTTCTGTGAGAGCTTATATCAGAAAGGCCACCGCAC
AAATTGCTGTTAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCCAGAACCAAAG
ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGAAATTTGATCAACTGTACTACAAGGCAA
GCCAACAAAGATTCCAACCTGGTACCAGTAAACGAAACCCAGAAAGAAACCTATCAAAGG
CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC
AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA
AAAAGATTGAGACGTTGATCGCTGCTGGTATCATCCGGAAGTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTADEYKQQGNAFTAKDYDKAIELFTKAI EVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPSWSKGYNRLGAAHLGLDLD EASNYKKALELDASNKAAKEGLDQVHRT
QQARQAQPD LGLTQLFADPNLIENLKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT
DPR LMTIMATLMGVDLNMDDINQSN SMPKEPETS KSTEQKKDAEPQSDSTTSKENS SKAP
QKEESKESEPEMEVDEDDSKI EADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN
RAAAEY EKGEYETAISTLND AVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTI EYYQ
KSLTEHRTADILTKLRNAEKELKKA EAEAYVNPEKAE EEARLEGKEYFTKSDWPNAV KAYT
EMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAI EKDPNFVRAYIRKATAQIAVKEY
ASALETLD AARTKDAEVNNGSSAREIDQLYYKASQQRFPQGT SNETPEETYQRAMKDPEV
AAIMQDPVMQSILQQAQQNPAALQE HMKNP EVFKKIQT LIAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA
GATATACAAGAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTCACTCTGTAGGTGTTCCAAATC
CTTCTGGCATTGACTTCTGTGCAGAAACCTTCAAATGAGTTCCACTTTACGTACAGATC
GCATAACAACCGGTCATATATTTTCTTTTGCTAAACCCCTACTGCAAGCACTTTTA
AGAAAAAGAACAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTGTCTTTCCGGAC
AAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCCTATATAAG
AAGGGCGCACATCGTCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG
TCAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA
AGGACTCTTGTCTATTGTGGGAGCACCTGCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA
AATGTGATCACAGCACCGGAAGCCCTCAATGTAAAGAGTTGTGGTGAAAAATGCAAATGCG
AAACCACGTGCAC TTGTGAAAAGAGTAAATGCAATTGTGAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECCKDSCHGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE
KSKCNCEKC

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTAAAAAATGAA
AAAAATTCATTATTCCTTTAGCGTAATTATTGAAGAAAAACAGTGCGCGCGGTAATTTTT
TGTCACCTCAGTAAC TAGAGAGAAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC
TCTGCC TAGGATTTCTCTTATGCTTTCCCTTTCACCAATCACTTTGTTCCGGCGAGGCCCG
CGAAGCTCGCTTCTTTT CAGCCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA
TGGCAGTTGCTGCACTTGCCATGAATATCTATGTGAAGCCTCTATGCAATAATCCAGTTA
CTGCGTTAGAATCCTGGTAAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT
TGATTGAAAATTAGTCCTTGCGACTTGGTATATATCTTATTTTAAGAAAGCTGAAAGGAA
GAAAGATCATCACGAACAACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA
CTGAATTGGAATTACAAGTTGCTCAAGCTTTCGTTGAATTGGAAAATTCTTCTCCAGAAT

TGAAAGCTGAGTTGAGACCTTTGCAATTCAAGTCCATCAGAGAAGTATGTTATTAATTTG
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAAGTGTGAACGGGACGATACC
AGAATGTTTCAATCTAGAAAAGTATAAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA
GTTAATTACAATCGGTCCAAGTTCTAAGCGGTGTCGTCCATGCATATATCATTTACAAGT
TACTGGCGTCAACTCTTCAAATATTTCAAAATATCACCTAATCAAACCTTACTAACATTTTC
CTTTTTTTGTTTTCTTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT
TTTTGTTCCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTGA
ATTGGAAAAGAAATTCCAAGACCGTCATGTCATCTTCTTGGCTGAAAGAAGAATCTTGCC
AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGC
TGTTTCATGACAAGATCTTGGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT
TAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCAAAGGATGTCCA
ACAAATCGACTACAAATTGGAATCTTTCCAAGCTGTTTACAACAAATTGACTGGTAAGCA
AATTGTTTTTCGAAATTCCAAGTGAAACTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

M SAPQAKILSQAPTELELQVAQAFVELENS SPELKAE LRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPT EIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGCTATTTGAGCCATAGTACCCATTAATAGGTCTCGTCC
ATTCCCTTGTTTTTTTTTTTATTGTTTCAATTACACTACATAATTA AAAATCACATCACTT
TCACTCTACCTTAGTCGTTCTTTATCAACCAAAAATAAAAAAATGCTTCAATCCGTTGT
CTTTTTCGCTCTTTTAACCTTCGCAAGTTCTGTGTCAGCGATTTATTCAAACAATACTGT
TTCTACAAC TACCCTTTAGCGCCCAGCTACTCCTTGGTGCCCCAAGAGACTACCATATC
GTACGCCGACGACACCACTACCTTTTTTGTCACTCAACGGTCTACTCCACGAGCTGGTT
CACCTCAACTTCAGCCACCATTACCAATGCGGCCTCCTCCTCCTTGTCACCTCTTCGGC
CTCTGGATCTGTAACCCCAAGATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC
CACTTTGCTGCTAACCCTTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG
TGTCAGTGACGAAGATTCAAACAACAAAGATGCAAAGGTCAAGTCTTTGAACAGGCTTC
AACTTCCAATGGTTGCGTCCCAATCACAAAGTTTGTCAGTGTCAACCAATGACCGGTTAC
CCAGTACGTTACAGTCAACCCCAAATACGACTACACAATACGTTACTGTCAACCGGTGCACC
TTCTGTTACCACTACCTCTCCAGGTAACGTACAATGGTACAACACCACTTCGATTACTAA
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLCLHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSLSLSPMSPLPSTLQSP
QIRLHNTLLSPVHLLLPLPLQVTYNGTTPRLRLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
990-1255 (SEQ ID NO 263)

AACTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCCCTAATGCA
AACACACGTCCTTTAAAGATCCCCTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATTTCTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTATTTCCAGAGAAGTACAATTTTAGGCGGGTTTCAAATTTCCCTGTGTG
CGAGAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCTTCTCCCCATTTCTATCAGCGC
GATAGGCATACTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACCTTAGATTAACTGGTAT
TAAGATTTTCGCAATTTTGGGCTGGATTATTAAGGTCGAGTAGCAAAGTTTAGCAAGAACA
GTACGAACCTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT
ACTTATTTCCAAGGTATGTTTAGAATAACTTTTCAAGGATGAAGATACACGGAAAGTC
AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTACATACAGATGTT
TCAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTTCGAAAGGACAGCACA
AGGCCATCGACCTGGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAAA

CGGTAAAACTGTTTTACGCGGAGATCCAACCTTTTGATCCTTACCGAGTACCACGAATCAT
CTATATGATCTTTTTACTAAGTTATCTTCAATTTCAACGGAGAGATGTAAACATCATTCT
CTCCTATGATAATTTCTTTTTTTATACAGAAGGTGTTGTTGTCGCCAAGAAGGATTTCAA
CCAAGCCAAGCACGAAGAAATTGACACCAAGAACTTGATGTCATTAAGGCTTTACAATC
CTTGACTTCTAAGGGTTACGTCAAGACTCAATTTCTCATGGCAATACTACTACTACACCTT
GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAACCTTGCCAGAACACATTGTTCC
AGGTACCTACATTCAAGAAAGAAACCCAACCTCAAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)

MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLR EYLNLP EHVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTCATATCTTAAGGT
GCTGATTGTTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAACAATAAATACGGTTTT
CGGGACTGTTTACCCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTTT
ATCTCTTTTACGGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
GCGGCCTAGACAGTTACTTCCAGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTCCA
AGTTTGTCCGCTAGTCTGTCTAGTCTTCTCAATTTTCCGCCAGATTCTGTCTAATTT
CTTTCCGCTCGAGTTGGCAACAGTACGAAGTAACCTAATAGATAGATAAACCCTT
TTTGAGGGCATTATTTTGCAGAAGATAATAGAAGAGAACCGTAACAAAGGAATCAAGCA
AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
TTTATATGGTGAGCTCAAATTGAATGAACATATCGTGGAATTTAAAAATACTGAAGAATA
CCCAATAAGTCAATGCAACCTGTGAATGTTTTCTTGAAATACGCCGAATACTGAATACG
ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTAAATACTGATGATATG
GTTAATATCATTTGAGAAGTCTTACATGAGGACTATAGAATACTACCATCCAGGAATTATA
GAGGAAATTAAGTGAATCAGAGATCTATTTTGAAACATTCAATTTACATGTAATTGTCTGC
AATAAAGCAATATTTTTGAAATATGCAAGTTTACTAACAAGAATAAATTTCTTTTGTATT
TTTATCTTTAACAGTGGCTCATTTCAAAGAATACCAAGTCATTGGTCGTCGTTTACCAAC
TGAATCCGTTCCAGAACCAGTGTTCAGAATGAGAATTTTGTCTCAAATGAAGTCAT
CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG
TGAAATTTGTTTCCATCAACCAATCAACGAAGCTCACCAACCAAGGTCAAGAAGTTCCGG
TGTTTGGGTTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA
CGTATCCAGATTGCTGCGTCGAAACCTTATGACCAAGACATGGCTGCTAGACACAGAGC
TAGATTTAGATCTATTACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA
GAGACAATACGTCAAGCAATTCTTGACCAAGGATTTAAAATTTCCATTACCTCACAGAGT
CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)

MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIAKSRYWYFLOKLHKVKKASGEI
VSINQINEAHPTKVKNFVWVRYDSRSGTHNMYKEIRDVSRVAAVETLYQDMAARHRARF
RSIHILKVAEIEKTADVQRQYVKQFLTKDLKFPLPHRVQKSTKTF SYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATATGTAAAAAATTTCTGCTTCATGTATATA
CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT
ACATCTTGGCATATTAAATGGTTATTTCCGGGTTTGTTCGGCTCAACGGTGATATAAAA
AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTTGTTTACAACATCTTC
ACATTTCCATTGTGGAATCATTTTATTTTTTTTTCAGAATACCTTACCCGCAAGCAAACTTT
CAAGCAAACCTTACAATTTGCAAAATTTTCATCGAATTTCTCCGCAGGACATATTATAAAAGT
TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCTTGTTCATTTGTTTTTCCCAAT
TCAAAACTCTTCACGGAGCAGTTTAAATTATCTTACTGTGCAAGAAGTCAAAAACCTAGACT
ATATATTAATTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA
CTGTTGTTGAACAAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTTGAGAA
CCGCTTTGGTTTACGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA
GAGGTGAAGCTTTATTGGTTGTTTGGTTCAGCTCTGTTACTGAAGCTAACATTACCAAGT
TGGTTGAAGGTTTGGCTAACGACCCAGAAAAACAAGGTTCCATTGATCAAGGTTGCTGATG
CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA
AGGTTGTCGGTGCCCTCCGTTGTTGTTGTCAAGAACTGGGGTGCTGAAACTGATGAATTGT

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVEEVVEVQEETVVEQTAEVETIEDALKVVLR TALVHDGLARGLRESTKALTRGEALLV
VLVSSVTEANIIKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTGCGACCAGATTGGGAATCTTACGA
CTATGCAAAGTTGGATCCAACCTAACGACGACGACAAAGAATTCATCAATAACATGTGGGC
CTGGGATAAGCCAGTTTCCGTCAATGGCGAACCAAGGAAATTGTTGACGGTAAGGTCTT
AAAATAATCTCTTTCGTACTATCCTTCATGTGCGCTTTTATTATAAAGTATGCTAGGTAGT
TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTTCTGCTCTGAAACT
TCCGCAGAAAAAAATCAAGTTTTCTTTTCGTATCTTGGATTATTGTTATATAATAGAT
GCATGTATTATATGTATAGCAGTGATTGCTTATTTTCTTGATTCTGAGGAATCGAAGAA
GTAACCTAGCGTTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATTTCTTAGGT
TACGGGGTTTTCTTGTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG
GGATACTGAATAACCTGTTAACCACATTGTATCCAGGACATTGTAGCTCGGGAACCACTC
AACAACAATTGCTGAAGACAAGATATCCGGATCTTCGCAGTTATTATTTCCGCCGAACG
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCTCTCAGTATATTCACTGTG
AGAATTGTGGCAGGGATGTGTCCGCAAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPD LRSYYFDPNGSLDING
LQKQQESSQYIHCENCRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
901-1605 (SEQ ID NO 271)

GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTTCATTCAGAGAAAACATCCGTACATTCGAG
TTCTCATTGAACCCATACATTTCAACTATTTTTACATAGTTCGTTTTTCATGTGTAAAAT
TGTTCATCGACGCCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCACT
GGGGCCGTGCATTTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCGTTCCCACTTGGAA
ATTGGCGTAATTCACGCTCCTCTATCGATTCTAGCGGGAAAGTTATCTCTCTGTTAAG
CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCAGTACCGACGTC
TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTTCATATACAGTGTTACCAAGGATAA
AGTGGTTAATGCTTATTCGTCAATTGAATTTTTATATTTGCTTAAGAGAAGTGACAAAAGA
GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA
GAGAACTTTATATGTGGAAAAATGGCATGAAAGTTTGAAAGTGAGAAAGAACTAAACAGA
ACCAGACGTCGTAAAGATTTTAGAAATTTTTATGGAAGAAGCAGGAAGACTACCATAT
ACTAATTGATGCGTTTGTGGCGTTATTTTTTAAACAAACAGAGCGGGTTACATATACTGT
TACTACAAACCGTGAAATTGAAGCAGTTTCATATACTTGGAGTATAGTCAATAAAAGACAA
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCTATTCAAACA
TTAATTTTGCAATAGTATACTAACAATTTTCTTAATAACCTGTTGAAAATTTAAATAG
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAGACCTTCGAAATTGATGATGAACAC
CGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCGTTGGT
GACGAATTCAAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA
ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAACGTTTCT
TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT
GGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA
GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA
AAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTTCGTGATTTTCGTCAACAGAGAAGTC
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA
AGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTCAGAAACGCTCAAGCTCAAAGA
GAAGCTGCTGCCGAATACGCTCAATTGTTGGCTTAAGAGATTGTCTGAAAGAAAGGCTGAG
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEV DGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAI VGPDLAVLALVIVKKGEQE

LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQRKRHQALQVRNAQAQREAAEYAQLLAKRLSERKAKEAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)
GTCTCAGTGATGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA
GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTCTTTTCAAGTTGTCTATC
ATCATGCCTTCACCTTTTGCCTTTCCATCTTTCTTTTGTCTGCAAAAATAAAGGGAAGAGGG
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAGAAGAAAA
AAAAAAAAAAGTAATCTTGATACCGTGAGCAAATAAGCTAACGGAAAGCGTAAGAAAGAA
GAGCGTGTTTGGGAAATAACACCACAGCATAAAGCTAAAATTACAGTTTATATAATCTAT
AGTAGTCCTATAGAAATTGCGAATAACGGAAACAATAGTCCACCAAAGCAAGCATAGGGA
GTGGAGATAGCATAGGTTATGATAACTAACACCGAGTTCGATGTGCCCGTAGATTGGT
TGTATAAAGGTAAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCTTCTACGTCCG
CAGCCTCCTCTTCATCTACGTCTCTTCGAAAAACGGAGACAATAGCAGCAGGTGTAACA
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCTATCTGTATCCAATGCAGCACTTTGTA
ATACTGAGAAACCAGATTTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA
ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA
GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAGCACC
CGCCAATTTCTTCACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGAGAGAAA
AGACTAAAAGGTCGATTTTGGATCTTTGTTTAGCAAACGGTCTACCTCTTCTTCAGCTT
CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCAGACTGAGAATGAGTCTGGTG
GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATACCAATGAGAG
GAGTGGCACCAACAGCTAGCAAGCCACAGACACCTATACTCCCTCCCTGCACTTGCAG
TAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGGCGTCGATAAATTCGAAT
CCGATCCTCCCCAACAACTTCCCTTCAAGAACCCCAAAAAAGGGAACATCCTTATCCCTG
ATGACATGATAAGCGAGGTTCTTCTATTTCCTGGGTATTTCAGTAGCAACCAATCCG
CCAAGTCAACCAATTCCAACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA
TACTCGCCCTGGAAAATCAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGTCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG
CAGGCGGTAAGCTTACTGAAAAGTCATCAGAAGGCACCATTAAGCAAGCAAGAGAGAGG
TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC
TCTCAAAAGCCGGCATTGATAAGCCCATTCATATGCATGAGCACTATTTCAGGAACCTG
ATCAAGATAAGTACCAAGACGGTCATTTCTATTGAAAATAACGAAGTTACGCTGGATGTTA
TTTACACAAGATGCTGCCATTTAAGGGAAATTTTACCCATTCCGCTTACCCTAAGACAAG
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTGTGAACCCTAAGCCTACCTTGA
TCGATATTCTTTCTCTTTTGTGATTTTCATCACCATTGCTCCCATTCACACGATTGTTTTCG
ACAATGTAGCTTTAAACCAGGATATGTTTCAAGAATAATTATTTCTGCTTTGGTAAACTCCA
CAGTTTGGACAAATTGAGTTTAAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC
TATGTAAGTTCTCTTTTGCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA
TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAACCTGTTTACTG
ACGTCTTGTCTCAGAGATCTCACAAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT
TTAGCAAAATTCCTTACTCATGCTTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA
ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC
AGGATTGTCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC
TAGCGTTTAAATGATCTGTCCACTATGATTAAGCCAATGGTTGGTAAACTATCTGCTCTAT
CATATGATAACTTAAGATATTTTCATTTTGAACAGCACTAATATTTGCACTTCTTATGATT
TAGCTTTGCTCTTGAAATATCTTTCTAAGTTGCCCTAACTTGATTTTGTGGATTGAGTA
ATTTGTGCGCAATGCTTTTCTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTT
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAAGGAAGTAGCTGTCG
TTTGTAATATTTTGATTAAAGTGCAAATCGCTCTCGCATGTGTCAATGACTAATCAAAACG
TTGAAAACCTTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAAACTAACACAGACG
GCGACTTGGATAGTTGAGACATTTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTCT
CATCCACACTTTACGCATTTGCTAGAGACTTCCAAACTTGATTGGTTTAGATTGTTGACT
ATGATTTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGGATGAGAAATATGA
AACGGACCATGGATTGCACTTTCCAGTTAGATGAATTGGATTGCGAAGATGATTGTCTAT
TCGATGGCTCTTTAGTAACTATGACCGCTGAAAGTGTTTTAGAAAAACTGAACTTGTAA
GCGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

TTGAAAAGTTCCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT
TGGAACAAAACCTTATGCAATATACTAGAATTGTTTTTCGCATAATCCGAATCTGAATGATG
TCCTTGGATCCAGCAGGGATGATTTCGAAGGAAAGTGTGACTCCAGCGAAGATTCAAAAT
TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAATACAACCTG
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAAACCTATTG
ACGTTTTTCACAGGCAAACCATTTGGTGTTCAGCATACATCATCTAGTACTTCTGTAGGTT
GTAAAAAGCAGGAAGAAGAAGAGGTGAACACATAAATGGGGTTTCTTCGTTTCAGCAGC
AGAGGTCTTTATACCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA
CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA
ACAATGAAACTGCTACCACTAGTTTATTATTAGCCCAGCTAATCCTAAGATTTTACCAAAAA
TTCCATCCGGTGTCTTAAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG
ATGATTTGATTTCAGAACGTTAACTCCAACAACATAGAATTGGAGAACATTTATGGTGAAT
CCATTTCAGAAATAGCGCTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA
ATACCGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTGTG
AAGTCAAAGTCACTGCTACCTATGACAAACTATTAAATAATTTGTCGATGGAGAGGTCAA
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLYKGKSRRTNTKPSRPSTSPASSSTSSSKNGDNSTSGNRSSNDKP
RARSSSVSNAALCNTEKPDLRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA
IDLIDNDDNGSSSTQFVRKKRSTISINAVVSSKPLASSAINATASSSVGKGKHPPISSPS
NATLKRSNSTSGEKTKRISIFGSLFSKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT
PDPRVKEISSPMRGVAPTASKPQTPILPSPALAVKDLSTVSLKRVSFVDFKESDPPQQL
PSRTPKKGNILIPDDMISEVPSISVGISSSNQSAKSTNSNIKGPLYTKKSKEYILALENQ
KLALREAAKHQEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPNVE
ADRELENNKLAENLSKAGIDKPIHMHYFKEPDQDKYQDGHSENNNEVTLDDVIYTRCCH
LREILPIPSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNQ
DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKLCKFLLLNKSLNKLDISQTKIKSDLAE
SLYRHNMDWNLFDTVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
RLGLAGATTSNISQDCLKFIFNWMSQYNVQGVDLAFNDLSTMIKPMVGKLSALSYDNLRY
FILNSTNISTSYDLALLKYLKSLPNLIFLDLSNLSQCFDILPYMYKYLPRFPNLKRIH
LDSNNLTFLKELAVVCNLIKCKSLSHVSMNTQNVENFYLMNGTDSFVQQTNTDGDLDSSS
TLDVKGQFAKNFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST
FQLDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKDTTKRYLLKKYIEKFHIL
HHNVQHTIDTMFEKRKSGELPLQEKENLVRLLLLEQNLCNILELFSHNPNLNDVLGSSRD
DSKESVDSSDSKLPALKHVESGYHVPEEKIQPENDVITARPHLMATDSGKTIDVFTGKP
LVFKHTSSSTSVGCKKQEEEEGELHKWGFVQOQSRSLYPENESTRQTPFASGDTPIINTET
AGKSTSSPSVSTSNNETATTSLSFSPANPKILPKIPSGAVLRS AIMKAKGIDSIDDLIQNV
NSNNIELENIYGESIQNSASTFTPGVSDSVAPNTDKGSVETLPAVSTDDPNCEVKVTAT
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC
TCAAACAGCATTTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCCTGTC
GGTATGAAAATTTAAAAATATATAAATAACATAAGTTTGCATTCATTAATATTAATATAAA
TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTCGCT
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA
TGTTTCTTTAACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG
CTGTGCAACATTATAAAGGTGCTTTTAAACTACTAATCGTATATTACGAGGTCAGAAC
GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCCGCCTTTATCAA
GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTTCAGTCTTCCTTTA
CGTCTTTAAGTAACCAAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAGG
GCACTAAAAAGGCAGCGTACCATCGTCAACCCCGAACACGAACATACTGCACCACCTTA
TAAAGCAAAACAAGACAATCACAAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTTAA
AAAAGAAAAGAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC
AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCCTTATTCATCAATCCCA
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG
AAGATTTAAATGAACCTCTATCACCATGGATTTCTCTGCCACTGGACTTGAATTCCTTTT

CAGAGTGGGAGAATATACCTAGTGAACACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAATGGATGAATTTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)

MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSKRKKGSKKAAY
HRQPPEHEHTAPLIKQNKTIKKEHSDVRGSHLKKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFHPPEKESMNTNELIHVSAKRNTLVDNKTSETLQRKMDEF SKRRGKGRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:
569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC
TGCGGTTCTTCCATCCCCATCTCTTCCACATATACCGGGGGTTCTGATGGCATTCCCTATA
GCTTGCTCAAAGTCTGCGAGTTTAGCTCATCTTGTGAGTTATTTGCTGGTTCTTCAACA
TTCGGAAGAGTAGTGTAGCCCCCTAGTATTACCACATATCCTTTGTATACTCATATGCGAAC
TTGTCTAATACAATGTATACCAAAAAATAACAGCTTGAAAAAAATCTCAGGGTCTTTTCAT
TGAATAATCTCATTTCTGCTATTTTAAAGTTTTTCGTTTGCAACCCGAGACTGTGAGCTAG
AAAATTTTCATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAACTTAT
GCAAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC
AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA
GATCTCTTTTGTGTTGATACTAACCAGTAAGTTGAGAGTTATAACAATGAAAATAGGA
TGCTGTGCGCACTTTTTTATCCACAGTTAGGTGAGTTCGAATTCATATATCATATTAT
CGCAGAACTAATCGATTTGGGCCATTCTGTGCTCATTATAACTCACGCTTACAAAGATC
GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA
TTTTTCAGAGAAACCACTTTCCCCACTGTTTTTCAACATTTCCAATAATAAGGAATATTC
TTCTCAGAGAGCAGATCCAAATTGTTTCATTCTCATGGTAGCGCTTCCACGTTTCGCTCACG
AGGGAATTCCTTCATGCTAATACTATGGGATTGAGAACTGTGTTACGGACCATTCACTCT
ACGGTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA
ACATAGATCGGGTTATATGTGTTTCTAATAAGTACGAAAGAAATATGATTGTTAGAACAG
AATTAAGTCCTGATATAATCTCAGTAATTCCCAACGCAGTGGTGAGCGAAGATTTCAAAAC
CAAGGGATCCTACTGGTGGCACCAAGAGAAAACAAAGTAGGGATAAGATAGTGATCGTGG
TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTCCGAAAG
TTTGTTCCTCACATGAAGATGTGCAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG
ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG
TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT
TAACAGAAGCAATTTGGTACAATTTAGTTGAGGCGCATCTTGTAATTTGCTAATTGTAA
CGACACAAGTCGGAGGAATTTCCCGAAGTGTACCAGTATGAGATGACTGTTTATGCAGAAC
AGACATCCGTTTCTGACCTTGTTCAGCAACAAATAAAGCTATCAATATCATAAGAAGTA
AAGCTTTGGACACTTCCTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG
TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA
AAGATTGGATGAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC
TTTATCTGTATGTGGAATTGTAGAGTACATGCTTTTTTTTCTCTTAGAGTGGCTATACC
CCAGGGATGAAATCGATCTAGCTCCAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA
AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)

MSSSHKVESYNNENRMLCDFFPQLGGVEFHIYHLSQKLIDLGHSVVIITHAYKDRVGV
HLTNGLKVYHVPFFVIFRETTFPVTFSTFPIIRNILLREQIQIVSHSGSASTFAHEGILH
ANTMGLRFTVFDHSLYGFNNLTSIWVNKLLFTLTNIDRVICVSNCKENMIVRTELSPD
IISVIPNAVSEDFKPRDPTGGTKRKQSRDKIVIVVIGRLFPNKGSDLLTRIIPKVCSSH
EDVEFIVAGDGPKFIDFQOMIESHRLQKRVQLLGSVPHEKVRDVLCOGDIIYLHASLTF
GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWM DVAKRTVEIYTNISSTSSADDKDWMMKMANLYKRDGIWAKHLYLLC
GIVEYMLFFLLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTTCGTGGAAA
ACCAGCATTTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT
GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAACGACTAAT
TCAACGTTGTTTTTATCAACCGAGCTTACTCTTGTACGGGTAACCGCAAGGATAGCTAGT
TGCGGATGGTATAGCGATTTGGCTGGCAGCATGATTAAGGAATCCAAACATCTAATGGAC
TAGCACATTCTATCGATTTACGGGTGAGGTAAACATAGATATTGGGATATATCATATATC
CTTACTGAGTAACTATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTCGA
CTAGTTCGAGCAAAAGAGTAACGCAAGCTTCAAAGGTTTTCGTAGAGTTTAAACACATG
ATGGCACCTTGGATAATGATTATTTTAAATAAGCACAACGTTTCTCAGAAATGCAAGAGTT
CTGATGCACTTTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG
TAAAGTCCAATCAAGGAAAAAGATCAGCATCTTTCATAGTCCGGTGCATAATACGCTGC
TCAGTCCAAAGAACAGCAGTCATTCTAATACTGGAAGTCTGGTTTTCGGCTGAAACCAC
GAAGAAGTAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA
GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC
AGCATTTAAATCAGAATGAATTACAATCCCGGATTCAATAGATGAACAAGAAGAAGATA
AATCAGGTACTGATGGAAAGGAAAAATCATAGAGCTGTATCCTTACCATTACCTCAATTAT
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA
CATCTCCAAGCTCAATTGAAACAAAACCTGAATGCAACAAGTGAATCAATGAAGAGGGGC
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAATTTGA
GGGCTTCATTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA
AAATTTCTGATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT
CAGATGAACAGTTTGATCAGGAAGATCACATTGATGCCCCCTAGGAGTAATTCATCAAGAA
AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACACAATTTATAA
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG
AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCCAGTCGACTGGAG
TTGAACGTAGATTTGAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG
ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAATTCG
GCAAGAGCAAGAAAAATGGTGGAAAGATCTCAACTTGGCCAAAATATACCGAACTCTCAGT
CTACTTTCCCCACCATTGCTAACATCGGTAGTAAAGATAAATAATGTACCACAGCACAACT
TTTCGACCTCCATATCGAGTTTAAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC
ATGGTTCAAGAATGAATAATATTTTTTCAAGAAAGGTAATCAGAATCTACTTCTGAGAT
CCAACGATCTCAACAAAAATTCGACCCCCGGCTCTCCATTGTCCAACGAACATATTA
CATCTAGTACGAACCTCCGGTAGCGATGCAACAGACAATCCAACCTCAGGTGCCAAATTTA
ATAGCTTCGCCCAGTTCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA
AATTATGTTGTCAGAGGGAGAATTCTATTATGGACTTAAGTTCACAAAATGACGGTAGTG
ACTCTATCTTTTATGGCAGGAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATTG
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGAGTACAAC
CTATAATAACGGGAAATGCAAATAATATCAGGAAAAAAAGCCATAACGATGCTCAGTCAA
TCGCACATTCTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTACTAACT
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTGAGGCAGTGT
TGTCCGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA
AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA
ACTTGCTGAGGGGCCGATGGGTTCCAGCACGACTTTGCACCACCAACGCGTCATTAAC
CTCTGCAGCCGACTACGAGGCGAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA
CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
YFNKHNVSQKCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKKSESTDEEVECFSEDNIEDGKVNNDKV
IAEHVMPEEKKNVQQLNQELQSPDSIDEQEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQKDGETSPSSIETKLNATSVINEEQSKVTKEADIDDLSSHSONLRASLVKA
GDNISEAPYDKEKKILDVGNLTAHKSNOQKPSHSDEQFDQEDHIDAPRSNSSRSKSDSSFM
SLRRQSSKQHKLLNEEEDLIKPD DISSAGTKDIEGHSLENYAPNMILSQSTGVERRFEN
SSSIQNSLGNIEIHDSGEHMASGDTFNELDGKLKRSKKNNGRSQLGQNI PNSQSTFPTIA
NIGSKDNNVPQHNFSTSISSLTNLRRAPESFHGSRMNNIFHKKGNQNLNLLRSNDLNKN

SAAPASPLSNEHITSSTNSGSDANRQNSNGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA
NNIRKKSHNDAQSIAHSSSDTDHKDEDDLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS
ESYLFNKDVNPINKNRTTSTNHSVGHTASQARNLLRGPMGSSTTLHHQRVINSLOPTTR
AVNRRMENVGYMHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTTCATT
TGTTCCCTTCCCTTATTTCTTTTCATAGTATTTATTTTATTTATTTATTTATTTT
GGATTTTATTTTATTTCTTTTAAATGCTAAGAAAGTAATCCGCATAATTAAACGTGTG
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA
CTTCTAAAATTCGCGCTCAACATGGCCGTATTGTACATTATATCGTCTCATATTATC
GTATACGCCCCGATTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACCTCGAACA
AGAGATCGCATAAAAAACCAAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA
TCCTCTAGAAAGGCAAACAGTAGATTTATTTCCCTTCTTTCTAGAAACATCATTATAACT
AACAATATATAATTGGAATAATGGCTGGTGGGATATTTTGGTTGGTGTATGTTATCAC
CCTGTTACGTTTTTTCGGATACTTAGTTTTATTTCAATGTGGTAAACATTGAATGTTTTCA
GCTTAAGATCTATTTTTTTTTTCTAGAAGAAATTGCGTCTTTACTAACTTTATTTTAC
TGTACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACACTCTT
TTCTTGGGTTTTGGATAATGCCGGTAAGACCACATGTCTACATATGTTAAAGAACGATAGA
TTGGCAACCTTACAACCAACATGGCATCCAACCTCTGAAGAACTGGCTATTGGTAACATT
AAGTTTACAACCTTCGATTGTTGGGTGGTCAATTTCAAGCTCGTCGTTTATGGAAGGATTAT
TTCCCGAAGTTAATGGTATCGTCTTTTTAGTCGATGCTGCTGACCTGAAAGATTTGAT
GAAGCACGTGTGCAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCTTTT
GTAATTTCTTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT
GCTTTAGGATTATTGAATACCACCTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA
GTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTTAGAGGCGTTCCAATGGTTATCT
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)

MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE
ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA
ELKDVPFVILGNKIDAPNAVSEAE LRSA LGLLNTTGSQRIEGQRPVEVFMCSVVMRNGYL
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)

TTCTTTACAATTCACCTTGCATTATTGAAGGAGTGCTATTCTTCGTTTTGCCACCCTTTT
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCCCTGCGACAGCGCAACAT
CCAACCTAATAGGTATGGGTGACTGACGATGCGATTATTTCAATTAAGTTCTGTCTT
TTTTGTATAAAAGAAAAAGACGGTGAAATCCATAGAAATACAGAGAGCGCAACACA
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT
TTCACCTTGCAGGGAATTATTGTTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT
GCGAAAGTTTCATTGTTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTCAT
ATTTTATTGTATTTCAACTAATATTATTTTTTTTTTTCAGTGGAAGGGAAGGTGAACCAAGA
ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAACCCCTATGCGTGATTGGAAGA
TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT
CCAAGGTTTTAGAGCAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCGGTATCAGAAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTTCGGTTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCCAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457)

TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTCTTTGTTCTTGTAAG
CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC
ACCGCTTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTTATTTCTCA
AAGTGATGCGAATTTTCAGAGAACACATTAACCTGGGGGCCATAAACGCGACGTGCTACCATT
TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT
ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTACT
TTTCGATTTCAATTTCTGACTGCATGATGCTTTTCTTAGGTAGTTTTTTGTTATTAATAAGTA
TCATAAATCTTGTCTTTTTACATAAGAATTAGGAAAGTACAGAACAAGAGCAAATTTAATA
TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTGAGCTGCTAAAGCTTCTCAATCTAGAT
CTGCTAAAGCTGGTTTAAACATTTCCGATTTGGTAGAGTGACAGATTGCTAAGAAGAGGTAAC
TACGCCCAGAGAATTGGTTCTGGTGCTCCAGTCTATCTAACTGCTGCTTAGAATATTTGGC
TGCTGAAATTTTAGAATTGGCTGGTAATGCTGCTAGAGATAACAAAAAACCAGAATTATTC
CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT
ACCATCGCCCAAGGTGGTGTTTTGCCAAACATTCACCAAACTTGTGCCAAAGAAGTCTGC
CAAGACTGCCAAAGCTTCTCAAGAACTGTAA

YBL003C, 132 aa (SEQ ID NO 458)

MSGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAA
EILELAGNAARDNKKTRIIPRHLQLAIRNDELNKLGLGNVTIAQGGVLPNIHQNLLPKKSAK
TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459)

TGAACGGGTGCAAAATTTACTTTAACACCCAAAAAGTATATGCGTATATATATATATTTATC
CTTGTTATTTTGTAAATTGAGCTATGCAACATAAGATTCCTGCGATGTAAGAATACTTGC
TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGGAAAAAATAAAAA
GAAAAAATTGAAAAAGAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT
TCTTGACATCATCAACACACCATCGCAGACCCACGTGGCCGCTTCGTGTGCCTTGAAAATAC
AGCCTTAAACGCAATCTCATTCGCGTTCTGTGGAATTTGTCTCGGACTACACGCTGGGCGTG
CATCACCAGTGAAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA
GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAACCAAACTGGTAAATAGGGCT
ACAGATGAGCAGGAAAAACGTTGCCGGAAGTTTATTTATCCGAGAGAATAATTGATGAAG
AAGTAGCGGTATGCACAGTAGCGCGGAAGTATTAGCAATTTTACTCTGGTGTGCACAGA
GTGTTTCATCATTTTTTTTACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA
GAGACCGTACCACACGTTTAGAGCAGCCAGGTTGCGAAACTCTTCTAAGATGGTTTCCAGCA
ATTGTGTACTATCAGAATGTGGACAGTTTAAAAGGTTGACTGCGAATTTGTCCCAAACCGTA
TCACCGTCGCATTTTTTTGAATTTGATCAAAGCACCCTCCTAATAGCACAGCGATGCTGTGA
GTGTGCCAGTGGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460)

MSRKTLPEKVYLSERIIDEVAVCTVAAEVLAIFTLVCTRVFIIFFTARICHGIWPSSPSE
PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLIKAPLLIAQRCCEC
ASNGNC

YDR529C, 884 bp, CDS: 501-884 (SEQ ID NO 461)

GAGTCTCCGGAGTTGACCAAGTCATACAATGTGCTACTGACCAAGAAATGGATCTGTGTAGT
TCCAAGATCGCATGCCAAGAGTGGACCGCCATTGATGTTAAACATTAACTCCACGGGGTACT
GTGGTATGATCCTCGTTAAAGACAGAGAAAACTAGAGAACCTCACTGAAGATCCTCATCTT
GTGGACAAGTCGTTACTGCAATGCGGTTTTCCCAACACAGCAGGCCAAAAACCAACAGAGTA
TCACTATTAAGGTCTATTAGCCATATGTACATTGTCTATAGATGTGTAACCTGCGCTGTGATC
TTGTTTTGACCAATCAGGAGCGACGCGCTTTTTATCGGGTCACCCCGGCGGGGGGCCTGACA
ATTTACTTTTCATAGAGCAGTAATAAAAGGGAAGAGATGTAAAGCTTGAAAAATAGCAGTA
AAGGTTGTTGTTGGACAATTTATCAGAATATTAGTAAGTGAATTAACGTTCCAGAAAGAA
CAAAATGCCACAGTCTTTTACGTCTATTGCGAGAAATTGGTGACTATATTTTGAAGTACCCG
TCCTCTCCAAGTTATGTGTTCCAGTTGCCAATCAGTTCATTAACCTCGCAGGTTACAAGAA
TTAGGGCTCAAATTTGACGACTTAATTGCAGAGGAAATCCCATCATGCAGACCGCTTTAAG
AAGACTCCCTGAAGATGAATCTTATGCCAGAGCATATAGAATAATCAGGGCTCATCAAACCG
AGTTGACTCATCATTTTACTGCCAAGAAACGAATGGATCAAAGCCCAAGAGGATGTTTCCTTAC

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT
AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462)

MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR
LPEDESYARAYRIIRAHQTELTHHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELNDNIE
VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTTTT
TTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCTGTGT
AGCCTAATGTTTAAATGCCTAATTTTTTTCTAAATGCAGCAACATACATATGTTGAGTCGTA
TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACATTTTAAAC
ATCCGTACAACGAGAACCATACTACTTTTTTTAATATTCTTTTTGTTCACCGCCTTC
TTTTTATTTTTATCCGAAGATCTTTTGGAAACCGCTCTGCGAATAGCGAAGCTAGGATACCA
AATTGAAACTTGACATAACTCATCTTAAAGAAGTATACTGTTAAGAGAGGCATTTCATTTC
GTGTATTATAACGTTTAGCATCAGTTACCTTGAAAGCCCAACATATACAAAAATACGCGTC
CAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTGAAGATCGAGAAATGGTCTTGA
ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTTAGAACAAATTA
TCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTGTCAGAACTTTTCGGTATCAGAAG
AAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTCCAAAGGCTGAAGAAATTTTGGA
GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAACTTCTCTGCTACCGGTAACCTTC
GGTTTCGGTATTGACGAACACATTGACTTGGGTATCAAGTATGACCCATCCATCGGTATTTT
CGGTATGGATTTCTATGTCGTCATGAACAGACCAGGTGCTAGAGTCACTAGAGAAAGAGAT
GTAAGGTACTGTTGGTAACTCCCAACAAGACAATAAGGAAGACACCGTCTCTTGGTTCAAG
CAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464)

MSTKAQNPMRDLKIEKLVLNLSVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN
EKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFSGFIDEHIDLGIKYDPSIGIFG
MDFYVVMNRPGARVTRRKRCRGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465)

GCAACATTACCACTTTGTACGGAGCGTCAGAAAGAAGCACCTCATCTATTATTATGAGAAC
GTACGATAACTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT
AATTAGCAGCAATTGAACACAAGGGATATCATTTGTGTGACCTTTGTTCTCTCATAGTTGC
TGTGAACCTTTAGTAACTATTAATGTTTATTTTCATGAGACTAGTCAAAACATTCAATAACA
GTTTTTCTATATGAGAAAAAAGCAACAGTACGATTATT
ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTGTGTACATTACACGAAAGAAAGAA
AGAAGCCTATTTCTTATAAGAGCAAACTGTTGATAAGTTTATAGCAAGAATAAAAAGGGTAA
AAAGTCATTGATAATAACCACTGCTGTGACTATATAATAAGAATCGAAGTGAAGTTAA
AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTATTTC
AACTGTGCAAGCAGATTTCATCAAGGAAAGCTCTTCTTTATTTTCGTTTCGACAAAGAGAGT
AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC
TATCGCTGTTTTTGAATTTGACAATTTCTCATTTATTGGACAACCTTGATGATTGACGAAGAAT
ACCCATTCTTCAATAGATTCTTTGCCAATGATGTCAGTTTAACTGTTTCATGACGATTTCGCT
TTGAACATCTCTCAATCATTTATCTCCATTATGGAACAATTTACTGTGGATGAATTACCTGA
AAGTGCTCTGACTTACTATATGAATACTCCTTAGATGATAAAAGCATCGTTTTGTTCAAGT
TTACCTCGGATGCCTACGATTTGAAAAAATTAGATGAATTTATTGATTCTTGCTTATCGTTT
TTGGAAGATAAATCTGGCGACAATTTGACTGTGGTTATTAATCTCTTGGTTGGGCTTTTGA
AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA
AGGGTAAAGAAGGCGACGATGATATTTTAAGCTCCATCTGGACTGAAGGACTACTAATGTGT
TTAATAGTTTCTGCGTTGCTATTGTTTCATTTTGATTGTTGCACTTTCTTGGATATCTAATTT
GGATATCACATATGGTGCCTTGGAATAAACAACCAATAAAAAAACAATTAA

YGR106C, 265 aa (SEQ ID NO 466)

MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDITISTISSTADVISSVDSAI
AVFEFDNFSLLDNLMIDEEYPFFNRFANDVSLTVHDDSPNLISQSLSPIMEQFTVDELPES
ASDLLYEYSLDDKSIVLFKFTSDAYDLKKLDEFIDSCLSFLEDKSGDNLTVVINSLGWAFED

EDGDDEYATEETLSHHDNNKGKEGDDDLSSIWTEGLLMCLIVSALLLFILIVALSWISNLD
ITYGALEKSTNPIKKNN

YGR182C, 854 bp, CDS: 501-854 (SEQ ID NO 467)

CCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAACGACTTAGCGAAGCT
TATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCATTACAGGTTACTAAC
AATGCATAAATTATGAGTAGTCTTTTTTCATCACTATATAAAACCTTTTTCAAACGAAACGCT
GTTTTTGGTGGTACTATCTTTGCAGGTGCCCTTTGTTTTCCAAACTGTATTTGATACTGCTAT
TACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGTCAAGGCTCGAATAG
CTGCAGGCGATGGAGACGACGATGATGAGTAAACGCTGATTATGTCACACATATACGTGCAA
ACGCTCTCTCTCTCTCAAGCTATATAAGTGGCACTCGTCTTATTTATTATTTTTTTTATTT
TGGCTGGTTGTTTCATGTTCAACCCAACCTCATAAAGGCACTCAACTTCATATTTTGACACAA
ATCTATGTCTCGCCAAAGCGCATTCAAATTTTCTAGAATGGAAATAGACACGAACGAGCTGTC
TGTCAGATGTTTCAAAAATCCTTATTATAATTTTATATTCTACTAAAGGAAAAAGAGAATTA
GGAAAAAGAATAACTCATTTTATGTATATACATATATTTTGTACATATCTATACCAAGCAAG
TATAGTGCAATACTGTTCTTCGACGTTATTAAACGTAATAGCATTTCCTTGGTATCCTTTGA
ATCTTATATACAAGTACGAGTACATACTGCGCAGTAAATTGATCCTGATGGTGTGTTTAGAT
TTCGCCAGAAGCGGAGGCGTTCTGGATTCTGGAGATGTAAGCCTTTGA

YGR182C, 117 aa (SEQ ID NO 468)

MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI
VQYCSSTLLNVIAFSWYPLNLIYKYEYILRSKLILMVCLDFARSGGVLDSDVSL

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-
914 (SEQ ID NO 469)

AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC
GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATATAAAA
ACTTATACATTATTAAACATTTGCGCGTCGATTGACTTTTATTTATTATTAACAAAGAAGTA
ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCTTATCTAGCGAAGGC
AACTTTTGAACCTCCCAAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGGA
AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCCTTTCCCTAATG
ACATCCCCTCTCAAACCTTTAGCTTAGCAGTTGTATTAAATGTCCTGTCACGGATAGTCAATA
ATCGTTGAAGGTTGATTTTCATATCCTTCGCAATTTTCGTAAAGCAACAATAGCAATACGGAC
TAAAATGGTATGTTGGTGTGTGTGTGCTGCTTACATTTTCAGGCTAAAAATGTTATCCGT
GGAATCTTCCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC
GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA
TTCAGGTTACTAACAATGCATAAATTATGAGTAGTCTTTTTTCATCACTATATAAAACCTTTT
TCAAACGAAACGCTGTTTTTGTGTTGGTACTATCTTTGCAGGTGCCCTTTGTTTTCCAACTGTA
TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT
CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470)

MSFSSLYKTFFKRNAVFGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD
DDDE

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 471)

GGGCTTTTCCAGTGCCGCGCCTCGAGATCCAGGCACCAGGAAC TAGGCACGCTGTGTATTC
TAACACATTGAAGGGCCTAGGCCCGCTGACGTGGGGTCTAGTTCCACTTTTTCATTACCTTT
TCTCGGTCTTTTCTTGCTCCACAGGCCGTTAATGGCCTGAAACAGTTTGTGACTTTGGAC
TTATGATAACGATGTTTGTCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCT
GTTTGCATCCATCAAGGCACTGCTCATTTGTGTAAAATTGTTCTACGCTTTTGTCAATCA
TATCTAAACTCACAGCCGCTAGGGTAGGTGTGCTGGCAGTGGTAAGGTAGCCGGCTCGTCT
TTGGTCATGCGCCAATACTGTGCAACGGCCCGCGGTAGCGTTCTTCGGCTTCAACCTTAGA
GCTGATACCTTTTGCTGGTCAAAGCGGCTCTTTTCGCTCTCGGTTGTAACACACTGTGACCTGCT
TTTCATGACTTTCGTTTCAAGCGGTCTCTTTTCGCTCTCGGTTGTAACACACTGTGACCTGCT
ATGCTTTTACCGTACTCGAAAAGCGTAGCCTCATGACTAGTTGTACCAACGCCCTTTCTTTT
CTTTTTTTTCTCTTGACACTTCGGCGTATTCATCGCCACTGGTACAAGCCGTATGGTGTCTTT
TTTGCTCATTTTCGTTTGTGACGTTGCGATGGTTTCGCGGACCAATCGCATGGGTGGTGGTGG
ATGTTGTCTTTGCTAGTTGCAACGTAGTCTTCTTCTCTCCTGCGCTTTCTGACGAAAATTGG
CCTTACGTATCTTTTTTTCGGCGTCGTTGTGTCATCGCTGTTTCATATAATCGTCGTCCTCA

TATCGGCGCTTTTACTGCATGCTGTCTTTTGAAGAGAGTTTCATTGAAAAGTAGTGAAGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAAAGCTTACATACGGAAAGAGAAAAA
AAGAAATTTTAA

YKR040C, 167 aa (SEQ ID NO 472)

MTSFQAVSFALGCNTLVACYAFTVLEKRSLMTSCTNALSFLFLLTLRRIHRHWYKPYGAFL
LIFVLTLRWFRGPiAWVVVDVVFASCNVFFSPALSDENWPYVSFFGVVVVIAVHIIVVTHI
GAFTACCLLKRVSLKSSEEKKKKKKKKKEKSLHTEREKKKKKF

YOL127W, 1343 bp, exon1: 501-513, intron1: 514-927, exon2:
928-1343 (SEQ ID NO 473)

TCTTATCTTGTATGCCCGATATAGCAACCTTGTGTGGTACCAATCTAACGGTTTCCGTA
GCAATGAAGAGATGAGGAGGCATGGGTCACTTATTTAATATGTACGGGTGTTTACATGGAGT
TGCTTTCTTTTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAGAGAAAACCGTGAGCCGAA
GTCCACGCTCTGGAGTTAGGCTCTCCATTACGGAGAGAAGCATTTCCTCAGCCTGGGAGCC
CCGTTGGAACAGTCAGGCTAAACTGGGCCTTCCTACCCACTGCTTGCTGTTTCTCACTGGAC
GCACAAGGGGATTTTCTTTCTACCTTCGGCTTGCCTCACTGCGTTGGGGCTTCCCAATGCAA
CTTCGTTTCGTATGCATACAATCTTTTAGATATTATCTTTTAAAATTATTTTAAAAACAATTTT
AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA
TAAAATGGCTCCATCTGGTATGTGAAGTGAATATTAATAGCACGAGAAAATTGAGAGGAAG
ATAGATGGGAAGTAGTAGAGTTGATATTGATGAGATACGAAAACCACACGTAAATAAACTAT
CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG
GCTCAACAGTTTATTAGCAATCGTTTGTATAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT
TACTACCAACAGCCATTAACAAATCCATTAGAGTGTTTCGTTTCGTTTCTGCTCAGATTCAA
GAAAATTATTCCATCCTCATTTACTTTTTTCTTCTATTTTCGTGCTCCACGTCGAGGTATCA
AGGAACATAGTTTACTAACATTAACGAATTCATCTCCTATGAATTTACTTTTTGTATAGCTA
AGGCTACTGCCGCTAAGAAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC
AGAAGTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC
TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA
CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTCCAAGTTTCCATG
AAAGCTAACAAATACCAAATCAAGAAGGCCGTCAAGGAATTATACGAAGTTGACGTATTGAA
GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT
ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474)

MAPSAKATAAKKAVVKGTTNGKKALKVRTSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV
IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV
RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTATTGAAGAGGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAATGCTTCTATGGCTTCTTTATTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAAACAATTCC
CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTTGGAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAAAATCATATCAATTTTATGTAATTATTTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGTATAACTCAACAATCTATT
ATTCCTAATTCTCAACAGGTGCTCTGGGCCAACTCACCCGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCTTCACATTTCATCATCGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCTGAATTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC
CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAATTACAA
TATCAACAGGGACACCAGTCAAGTTTCAACACCTACATTGAAATCTTCTAGTGCTGCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTGTGATGTGAGATCCACACCTCCCAAGTAGTTTGTGCT
CAACAGCAACAACAACAACAACAACAGCAACAGCCGCCACTAACTTCATCAATCCATGATTCT
CCAACACCACATCATCATTTTACCATTCAACAGCAGCCACCACAACCAATCATTACCTATCCAAT
TACCATCAGGGGGTTGGATCTCAACCAAAAACCTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)

RERIEEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSTHTERMFLNLPFNNS
SFNAPPVEINFNDLEVLELYTQLVLRYDDITKSTFELAI SPANLNISQRKIIISILCNYLNLELFD
NGLIIIRKPGYIAQCITQQSIIPNSQQVSGPTHPPQHQQNQLOQQQQQHQHQHPSHSSMMNLH
QLGGTLAVPAHPELLRSQSQSALPLPRLRQQTSTPIQQNQVQHQNQPPQQQQQHQVQPOYNYYNQ
QSIQSOPHSARPYSQSYNIYQQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQGVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

ATAAACAAAAAGAAGCACGAACGTGGGCAACAACAACAACAACAACAACAACAAAAAATTT
CTGGAAAATCAAATTTGAACCTCAACCAGCAGCGGCGGCGGACAGAAAAATATATTAACAGAAT
ACTTTTTTGTATTCAACTCTCTAACTCTTTCTATTTTTTTTTTTTCTATATACACTGTTAAATC
AATCAACAATAGCAGGATATCCATTCATATACAAATAGATAAACTGTTTAATTAATTAATTAACCTG
ATTTGATTTGGGAAAAAACAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAAACAATTC
AAGCTTTAATTTCCACCTATCAAATTTTATTATTATTTTGTTCATTATTTTTTTTCCCTTTCT
TTTCTTTCTTTCTTTCTTTTGTGAACAAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC
CGAATCAAATGGGCACTGTAATGCAACGTCGTCCCTCTCTATCATCATTCATCGTCAGCCTCGGGCT
ATTCTTCTTCCAATTATGGTGGAAATCCTACACCCAATCCCAACAATTCCAATACCAATAACAATA
GTAGTGGCAATAGTAATAACAACACTCATGGCAATAACACTCCCAATTTATCAACTCAAAGATTGA
CAAATAATAGGAATTTACAATCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAACAGCAACAACAACAACCTTGATCTGTTGGAAAATAATACTAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCAACCCATGTCAACACAAATGTTAATGCAACACAACAGCAA
CTAGTATTAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA
AAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACA
CTAACAATAGTAGTACAGGAAGTTCTAACATTGCAACATGCTTCCTTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATGACACCACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCATTTGCCATTAAAAAGGAACAATTGT
TAGATGTGATGACAAAATTAACTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

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TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG
GTTTATTGGAGCCTCTGAATCGTGCCTGGTTCACCTTAGTTTATTGGATAGAGAATTGGAAAGATTAA
GATTTAAACTTCAATTTGAAGAAGGGGGGCCAATTGAAGTATATTATTTGTATATTAAATTGATGA
TCTGCTGCTTTGCCCTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTTCAT
ATTTATCAGCAACAAGAATCGTGACAATCGTTTCTAAAATGGTGAATGACATTTTCATTGATTGAAT
TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTCATGTTGTTCAAATTACATTTGTCAA
GATATTTGATTGACAAGTATGTGGATAGTGCTAGACAGCTGATTGTTACTGTGCATCGTTTATTTA
GAAACACGTTGAGTTCCTGGAAAGATTTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA
ATTTGAACATGGTGTGTATAATTATCCTGAAATATTTTAAATGATCTGGAAAATGAGGATTCAA
GTATTATCACCAGAATGAGGTCACATTTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC
ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAAAGAAAATCT
TGCCCTTGCCATTTTACAACCAAATCATAAGGATGATTTCAAGACAATTACCACGACATCACCTA
ATGGAAC TACTATTACTACATTAGTTCCAAC TATGAATCAAGCAAAACTGAAATCTT
TTGATTCCAGCAAACCACCTGAAATAAATGGTATTCCTTACCTATGCTTGAAGCTACTGGTTCAA
CAAGAGAAGTTTTAGATTCTTTACCCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT
ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAAAAGCACCTGCAGC
AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC
AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC
CTTTTATTTTGGCAAACCTACCGTTACCACAACTTATTTGCCAAAGATTGATGAAATGAATATGT
CACCAGAAGTAAACAAGAAAACCTCTGTTGCTCCATTTGCATCTCAAATCACCAACTTTTTTGTATC
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTTGGGTTGGTTTGATGTTA
ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLPAQTKPVNSKRKSAASTPGNESKKSRKSNSTASTPNSA
TPTSVGTTPPQKTSKPTGHRPVTSCFTCRQHKIKCNASDNYPNPCERCKMGLKCEIDPEFRPRKGS
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYTSA
NSSPQVAFSNASPIPSVTSIQQNAPLTHENS DNSPYALNTPENIEELQPISEFILGDVTLPLNRAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQGLHRGGEFIQEF SRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLL ENARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGLLEPSNRAGSLSLLDRELERLRFKLQFEEGGPIEVVYLYIKLMICCF AFLPGTPIE
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLMVLYNYPEIFLNDSENESSITRMRSHLTSA
LFYDLVWCVHEARRRSVLDKGRQAQPNKKILPLPFYNQITKDDFKTITTTSPNGTTITTLVPTDQ
AMNQAKSKSFDSSKPLEINGIPLPML EATGSTREVLDSLPSQSLPSQAPTLOQYPMQDQQQQEPS
QQQQQKHSQQSQYQQQQQSNQQQPHLQHQRQFQQSPPPQFSMISSTPPLQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVAPFASQITNFFDQQTSGWFNNDNQDDDFLGWFDVNMMEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTCTATGTCTCCGCTTACATCACACATCATACGTTT
GAAAACACCCACCCCTTTTCTTATCTACAAAAAAAATAACAACTCACTATAACTACTAAAC
CTTTTTTTTTTATTTATTTATTTTGTATTTTGTATATTAATCAAAC TATTATCATCTATATA
TACATCCCCATCGATTCATCTGACATAATAGTATGTATGATCATACAGAGGGGAAAATCACCTTTT
TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTGTGTAG
ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAAATAATATGGAAATAATACTAACAGA
ACTTAGAAACATCACTCATAATGAGATCACAATTCAAAGACGAGCATCCTTTTGGTATGTATTACA
TGATTTTTAGTCCTCTGAATCTTCTTCCGATCATCATATACTAACATTTTTCGTGGGTGTTATTCCTT
TAATAGAAAAGAGACAAGCCGAGGCAGCCAGAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA
TCTGTGAAAAGGTTGAGAATTCGGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG
ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAATCAAGTTACCAAGCGAAAAAGCCA
TTTTCATCTTTGTCAATGACATATTACCCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC
ACAAGGACGAAGATGGTTTCTTATACGTTTTTACTCTGGAGAGAATACTTTTGGCGAGAACTAG
CAATTGACATTTTCATCATTAGATTTCAAGTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAAARIAQRFKDRVPVICEKVENSDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIEEHKDEDGFLYVLYSGENTFGEKLAIIDISSLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

GTGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGGTATTGCTGTGCATACGATACAAAAA
AAACAGAAACGAGAAAAAATCGATCGTCAACCTTTATCAACTCATCTACAGCAGCAGCAAAGTT
CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT
ACTTTCATTTTCCATTTGTTATGCTTACGACAACTGAAACCATGCTACTTCATACGTTTGTATTGA
TGTTTGCCCTATTGGTTGCCATGGGATCTACGCTTATTGCTTCAAGTATCATGTTTGCAATCT
CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT
GTCTACTTAGTTTTATAGTTTTAAAAATTTGTTAATATAAACCCAAAGTTTCTAACAGGCTCTGTTT
GCTCGACTAAAAAGAATTTTGTCAAACGCGTATCAGAATGTTTACCTTTTTTTTTTTTACCACAG
ATCAAATGAATGTTTCGACCTAATGCTCCGTTTCGGCCTCCTAGACCAATAAAGGGGGGTGTTGCGG
TGGTGCAGAAAGTAGTAAACGAAAAATTGCCCACTACCACCAATCCTAAACCTGCAAAGATTTTGA
CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAGAAACTTCAAAGAAGAACAAAA
CATGGGACGGTGATGGGTATGCCGTGATTAAACAGCTTGAAGATGGGGCATGCGAGATATCTATCA
AGAAGCTCTGATGGCAAACCTATGGGGAAGAGTGTCTTACTGCGACACCTAACCTTGACGACGTGA
TTAGTGTGGGACCCTATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG
TGACACGTGTTACCCACCAGTTCAAAAAGGTTGCTCCTCCACAGCTAGTAGTCGGAAACCGCTTT
ATGACGACTGTGCCGATGCCATCGCGTTGCCTCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA
ATATCGATCCACATTTGGCAAAGTGCTTCGTCCGCATCAGGTTGAAGGTGTGAAGTTTATGTATG
AGTGTTTAATGGGGTACCGTGGGTTTGGCGGGCAGGGGTGTTTGTAGCAGATGAAATGGGGTTGG
GGAAAACGTTGATGACAATCACTACAATCTGGACGTTGCTCAAACAAAACCCGTTTATGGAAAAAG
GTGCAGTGGTAAATAAGGTATTGGTGGTGTGTCCTGTACGCTTATTTCCAATTGGAGACAGGAGT
TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCAAATGTCAAACGAGA
AACAGGATATACTCAATTTTGGAAAGTTGAATGTGTACCAAGTGTTAGTGGTGAATTATGAAAAAC
TTGTGGCACATTTTGATGAACCTCTCAGCGGTCAAGTTTGAATTTGTTAGTGTGTGACGAGGGCCATC
GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTCCGAAGAAAATTG
TTTTGACGGGTACGCCGATTCAAAACGAGTTGGTAGAGTTTCACACGTTGATCTCGTTTCTCAACC
CGGGTGCTTCCCGAGCTAAAATTGTTTCAGCGAACTTTATAACACCTATATCTAGGGCCCGAG
ATATCAACTGTTTTTGACCTGAAGTGAAGAAACGCGGTGAAGAGATATCGCAGCAGTTGATTGAAT
TGACTCAGAGTTTTATTCTTAGACGTACACAAGCGATTTTGGCTAATTACTTGACACAGAAAACCTG
ACATTTTGTGTTTGTTCACCTACATCGTTGCAGCTCAAGTTGTTTCGACTATATAACCAACTTGA
AGAAATTTAATCAGTTTGAAGCATTTACCATGATCAATTTGTTTAAAAAGATTTGCAATTCCCCTT
CGTTGTTGGCCGACGACGAGTTATTTAAAAAGATTGTTGAAGAAAAGTTTAAATTGGGGATGGCAT
CCGGTAAATAAACATTCTTGTGCCGTTGCTATTGGAAATTGCTTCGCTTGGGGAAAAGATTGTCT
TAATTTCCAACCTACACCAAGACTTTGGACTTGTGGAACAGGTTTTGCGCAAGGTCAGCCTAACAT
TTTCGAGATTAGATGGGTGACCCCCCAACAATGTGCGTAGCAAGTTGGTTAATCAGTTTAACACGA
ACCCCGACATAAACGTATTTTATTGTGCTCGAAATCTGGCGGGATGGGGATCAACTTGGTCGGGG
CTTCGAGGTTGATTTTGTGTTGACAATGACTGGAACCCAGCGACCGATTGCAATCGATGTCGCGAA
TTCACAGAGACGGACAATTGAAACCGTGTTTCATTTATAGGCTATTCACCACGGGGTGTATTGACG
AGAAAATCTTTCAGCGACAGCTCGTGAAGAACAAATTGAGTTCCAAGTTTTTGGACAATGACGCCA
CGTCCAAATCTGATGTGTTTGACAATGATGATTTGAAGAATATTTTTGAGATAGATACATCGACAA
TATCCAATACTCATGATTTATTAGAGTGTGTGTGTGAGGGCGACGGGTCGATTGTTGAGTCAGCCAA
CCATAGAGGAAAGCGAACCACCCCAACAAGCATGGGTTACTGCATTAGAGCTTAAGAAGAAGA
TTGACGATGGTGAGGCGCTAAAGAGGACGGCTGTAAATTTGCCTTGAACGATTATCGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTTTGAATCTGCGCTACACCGAATTGCTAACAAATTCAAGCT
ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACTAATTAA

YBR073W_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRIKGGVAVVQKVVRKLPTTTNPKPAKILTTDPGSTKYVIQW
RKKTSKKNKTDWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTTIWTLKQNPFMKGA VVNKVLVVC PV
TLISNWRQEFKWL GANKLVLT LNNPMSNEKQDILNFGKLVYQVLVVNYEKLVAHFDELSAVKF
DLLVCDEGHRLKNSANKVLNNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPKLFLQFN
FITPISRARDINCFDPEVKKRGEEISQQLIELTQSFILRRQTQAILANYLTQKTDILLFVPPTSLQL
KLFDYITNLKFNQFEAFTMINLFFKKICNSPSLLADDELFFKIVEEFNLGMASGKINILVPLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVS LTF SRLDGSTPNNVRSKLVNQFNTNPDINVLLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMSRIHRDGLKPCFIYRLFTTGCIDEKIFQRQLVKNKL
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLLECVCEDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDDGEALKRTAVKFA LNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

AAAGAAATTTCAAATTTAGTTTTAGGTGATAATTATCGTTCGTCCTTTTCCTAACCTACCAATTTTGA
CTTTGTGTACTCATACGATGGTTGTTATTAGTTAAAGTTGCTTTGCTTTGCTTTTCAATTTCAATT
TCACAATTGAATTTT CAGAATAGAATTAGTTT CACCTTTTCTTACAATCGGCTAAGATTTTTTTTCA
TTCTTCTAATTTAGTTTACAGAATAGAAAGAATAGTTTGCTTGTTTGCTCATATTTACAATCAATT
GGTTATTGGTGTTTATTATTTTTTTTTTGGTTCCCTCTTTTTACCCCCCTTCCGTCTAATTGAGTTA
TTGTTTGGAAATAATTTACTTTCAATATATTTTTTTCTTCTTCCCTTCTTCAACTTCTTC
TTTATACATTTCAATCAACCTTCCAACAATCCTATAATTACTTACTTACCTTCTTCAATTGGATTA
ATTGGATTTGAATTGTTACAATTGAATACTTCAACGAGATGACTTTACCAATTCAGGATTTAGAAC
CTGATTATTATATTTCCGTCAATTATCCTACCACCGATAATGGATCACCAACCCACAAGCTGAAA
AATCATTTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCGCCCAAATTAGACCTGGTG
ATTTAGACCATTTGTTAGTCTTTGTTAAATTGCTTTCATACAAGTTTTCTGAAGAAGCTGAAAAAG
ATTTAATTA AAAATTAATGAATTTGGTGTCACGGGTAAAGATGACGTGTTAGCTTCTAACTTAGAA
TTATTATCAATACTTAACCTATCCACAATCAGTTGGTGGATGTGGTATTACTCCTAATTCTGGGG
ATTGAAAATTTGTCACCAGTATTGTTCCAATTACTAATGCCTTTAATGAAACCACTTTAGTTGAAG
ATTTAAAAATTAATGTTACTCAACCAAATTTATCAATTGCCACTATCAAAAAGACATATGGAGTTG
AAGTTGCTCTTTATTTTGAATATATAAAACATTACACTTTTTGGTTATTATTGCTTTCTATTATTG
GTCTTGATCTCATTTTTAGAAAAGATAAACGATTCCTGTTAACTTTTGCTTTTATCAATTTGCTTT
GGGGGGTTTTATTCCTTGCATCATGGCATAGAAAGAGAACAACATTTGGTTAATGTATGGGGTGTTT
AAAATAGTCATTTAATTGAAGAACATAATTCCGAATTGGCTAAAGTCAATGAAAGATATGAAGAAA
AATCAACTTATTTCCATGCAAATAATACCAATGGAGTTAGATTTTTTAAACAATTTGGCATTATCC
CCATTGCCTTGTGTTGTTGGTGTTTGGATTAGTTATCAATTGAGTTGTTTCTGTTTGAATCT
TTTTAACCGATATTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTTAATCA
GTGTATTTGTGCCAATTTTGACCATTTGTTTATAATGCTGTCACGGATATTATTATTAATGGGAAA
ATCATGATAACCAATATAGCAAAAATAATTCTATTCTTGTTAAACCTTTGTGTTGAATTTCTTGA
CTGGTTATGTTCCATTAATCATCACTTTCATTATATTTACCATTTGCTCATTTGGTGCAACCTC
ATTTAGGTGATATTA AAACCACTATTGCCACATATGCTGGTGAAATAGATTCTACACCAAATACT
TGTTGAAATTAAGAGTCAAGAAGAATTTAAATCAATCAAGGTAGATTAGATGCTCAATTTCTTTT
ATTTCAATTGTCACAAATCAAGTTATACAATTGGTATTGAAATATATTCTCCCATTTGGGTTTAAGAT
TTGTATTTAATTTTATTGAAACGAAATTCAGAAAGAACTCAATTACAAACTAAAGATGATAACC
CTGATGAATCTATTTGGTTACATAATGTCAGATTATCGTTGAAACTTCCTGAATATAATGTTGATG
ATGATTTT TAGAGGATTAGTTTTACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG
CACCATTGGTTGTATTATTTTCAATTTAATTTTTTTCAAGTTGGATAATTTTAAATTATTGAATG
GTAAATATTTCAAACCAACAGTTCCAAGAAGAGTTGATTCTATTCATCCATGGAATTTAGCCCTTT
TCTTGTTAGCATGGATTGGATCAATTTATTTCCCGTGGTCACGGCATTTTACCGTCATGGTACTG
CTCCACCAAAATCTATGGGTCAATTTGCCCTTGATAAAGCTAGTGTTCATGTTTCATCCTCAGTTT
TCTTGTTTTTATTAATGTTTGTTCAGAACATGGATTTTTGATTTTGAGTTATCTTTTATTGAAAT
TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAATGATTTTGTTGATAATGATATTAATTTGA
GACATGATTATTATTCTGGGAAAGTAAACCAACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA
AGTTTACCCCAATCAACTTTGAATTTCACTGGTCTAAACCAACCGCAGAACTGATGATAAAG
TTGAAAAAATTGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTACTGCTA
CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLPIQDLEPDYYISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLHLLVFKLSS
YKFSEEAEKDLIKNYEFGVTGKDDVLASKLRRIYQYLTYPQSVGGCGITPNSGDWKFVTSIVPITN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVFLASWHRREQHLVNVWGVQNSHLIEEHNSELAKVNEREYEEKSTYFHANNTNGF
RFLKQLAFIPIALVFVGVLSISYQLSCFCIEIFLTDIYDGPGLSLTLLPTVLISVFPILTIVYNA
VTDIIIKWENHDNQYSKNNLSILVKTFVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLKSQEEFKINQGRLEDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLHNVRLSLKLPEYNVDDDFRGLVLQFGYLIMFGPVWPLAPLVCIIFNLIFF
KLDNFKLNGKYFKPPVPRRVDLSIHPWNLALFLLAWIGSIIISPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVDNDIKLRHDYYSKVKPTY
KVHSDDELWEKFTPQSTLNF TGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399..1781 (SEQ ID NO 297)

CGGTAATTATGTACAAAAACAAACAATCAACATATTAAATCGTTATCCCAACTTTGTCAAGTTTAA
CTAACACCTTTTATTTTGTGTTATACAAATTGCACAATCAATTACTATAACTTTTTTTTGAAACGT
GGGCTCTGTTTAGTTTAACTTCTTGTAGTTTATTATTCCGATTGGGTTAGCTCAATAACTGCATT
TCGTACAATAATGTTAATTCATTTCTAAATTCGATGAACCGAACACACAAAAACATCCAGTTCT
GGAGAGATTTTCAAAACTTCTATTATAAATAGAACCCCTATAAGTCCATAAATTCATTTGAAGG
ATTATTTTCTTTTCCCTTTTCTGATTACTTTTACCAATTTTCTTCTCTCCAAAAAAACACCTTCT
TCATGGTTTCTGTTTCTAAATTAATCAATAACGGGTTGTTATTAAGTCAAGTGTTTTCCAAG
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG
CCCCTTATATTCAAAGAAACGGATATGGGATTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTC
AAATTCATTTGATTCAAGACATGGTGAAAGATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAACTACAAAGGTACTTTTAAAGGTGATTGTCAATTTCTTAAATGATT
ACACTTATTTGTCAAAAGACCAGAGTAACATGCTAAGGAAACTAGCCCAAAAAATCTTGAAGGAA
CCTATGCCGGTACAACCAATGCCTTGCGTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT
ACAAGGAAAACCTCAACTTTACCAATCTTCACATCCAATTTCTAACAGAGTACATGAACTTCAAAGT
ATTTGCTAGAGGGTTTGTAGGTGATGATTATGAAGAAGGTAAAAGTGTCAAGTTTAACATCATCT
CTGAAGATGCTGATCTTGGTGCCAATAGTTTGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAAC
TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTAAATGCTATTGCTGAAAGATTAGTTA
AACCACACCCAGGTTTGAATTTGACTACAAGTGATGTCAACAATTTATTCAGTTGGTGTGCTTTATG
AAATCAACGTCAGAGGAAGTTTCACTTCTGTGATTTATTACCAATGAAGAATTCATTGAAGAAT
CTTATGGTAACGATCTTTCCAAATATTATTCTAATGGTGCTGGTAATAATTACACCAGAATCATTG
GTTCAAGTATTTTGAATTCATCTTGGAACTTTTGAAGGACACTAAGAATCTAATCAAGTATGGT
TATCATTTGCTCATGATACTGATTGGAATTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTG
AAGATTTACCAACATCTTACATCCCATTCCCTAACCCATACGTCATTCTTCTATTGTTCCACAAG
GTGCCAGAAATATACACAGAAAACTTCAATGTGGAACGATGCTTATGTTAGATACATTATCAACG
ATGCTGTGCTGCCAATTCCAAATGTGCTACTGGTCCAGGGTTCTCTGTAAACTTGATGATTTTG
AAAATTTCTGTAAAGAAAGAATTGGAGATGTTGACTTTGTTAAACAATGTGGTGTCAATAGTACCT
ACCCATCTGAGCTTACTTTCTACTGGGATTATAAAAATGTCACCTTACAGTGCTCCTTTAGAATTGT
AA

YBR093C_homolog_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPKSNKSLKSLAIYAKFENYKGTGKDLNFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLLEIFHSALGLLEPAEDLPTSYIPFPNPVYHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSSELTIFYWDYKNVTYSAPLEL

YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871;
CDS: 501..1868 (SEQ ID NO 299)

GAGTTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAACCAAAT
TTATTTAACGATGCAATAATTATTTCATGTGAGCTATCCATGAATCAGTGAGAATCTTTATTATG

GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACTTTATATCTTGGTGTGGGATGGTGCCACA
AATGGAGATTGTTGAGTGACATGAAAAATACGTAGTTAAATTTTGTTCCTTGTTCCTTATTATT
GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAAATTACGGGGATTTAATTCG
CGACTCACCCACGTTCTCACACAGTATGTGCTTTTTCATAAGTATGATTTGAACCTTAAATATC
AACTTTCATAAATAAACATAATTCCTTCCAGACAACTAAATGGTTGGTTTATCACGAGTACTTAATG
CTGGGTTTATTCTAAGTGACAATCTGTTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG
AACAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAATTCAGGGTATGGGA
TTTCTACTGATATACCAGAAAAATGCACATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC
GATTTCCCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTTCAAGAGATATGGTG
AATTTTCATGGAGATTTATCTTTTTTAAATGACTATGAGTATTTTCGTTACTAATCCAGATTATTATG
AAAAGGAGACTACTCCTAAAACTCAAAGGTCCATATTTTGGAACTACAAATTTATTACGACATG
GAGCTTATTTTAGAAAAAGATATCAATCACTATTTGACCAAAAGGAGAAGCTTGTGTGTTTACTA
GTAATTCCTGGAAGGTGTTATCAAAGTGGTGTCTATTTTCGCTCGAGGATTTTATAGGAGATGATTACT
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAATGGGTGGTAATTCATTGACAC
CAAGATACGCTTGTAACCTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA
CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC
AGGTCTCGTCATTATTTCTTTGGTGTGCCTTTGAGATTAACGTTAGGGGGTATTCTCCATTCTGCA
ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA
CTGGTCCAGGTAATAATATGACAAAGGTAATTGGCTCACCTATGGTGGAAGCGTCGTTGAAAATGC
TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGATTTTGACAT
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCCAATCCATATA
ATGCAGCAGAATTTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTGAAATGTGGTGAAAAGC
AATATGTTAGATTTATTGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGAGGTCCTGGGT
TTACTTGTGAATTGAATGATTTTATCAAATTAGTTAAAAGTCGTTTACATGATGTTGACTATAAGC
TTCAATGTGAAGTGGACGGACCGGAATTGACATTTTATTTGGGATTATAAAGACAGAAAGTATA
ATGCGCCGTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMISRHERFPSKGDGKYFNSVMEVFKRYGEFHGDLNFLNDYEFVFNPDYIEKETTPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRQYQSGVYFARGFLGDDYSEDTFEVVVVDED
KKMGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPGDLDSADQVSSLFLWCAFEI
NVRGYSFPCNLFTKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASLKMLQEDSKIWLTFTH
DTDIEMYLTSGLLIVPPGDLVPDRVPFPNPNYAAEFFPQGARTYTEKLKCEKQYVRFIVNDAVYP
YPDCSGGPGFTCELNDFIKLVKSRLHVDVYKLQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
CDS: 500..1885 (SEQ ID NO 301)

TGTAGTATAAATAAGGGTATGAAATACCAACATCCCAGAATATCAACGAGATAGAAGAGAGGAGTT
TCAATATATATCTTGTGAATAATAACTTCGTTCTAATTCACTATACACAACCTAGACGTGTACACGC
TCAATCTCAGGTAAAGAAAGTTTATATTCCATCACTATATAACAACAATCAGGCTTTGCAAAAAA
CATTTAAACTAATACTGGTAATATGGAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT
TATCTATTTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAT
AAAAATAAGTAATATAAATAGGTATGCATTTTCCCTACATTTATTTCTCTTTCTATTTTAATTTG
TTTCTTAAACAGCAACAACAACAATTGAAATTCAAAAATGGTTTCTGTTTCTAAATTTATTGAACAA
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
ACAATATAACATCGTCAATCTCTTGGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGAT
TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAAATGTATTCAAGACATGGTGAAAG
ATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACCTACAAAGG
TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATACTTATTTTGTACTGATAAAAACAATTA
CGAAAAGGAAACTAGCCCAAAAAATCTGAAGGAACCTATGCCGGTACAACCAATGCCCTTGGCTCA
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTCACATTACCAGTTTCTC
TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGCTAGAGGATTTTATAGGTGATGACTT
TAAAGAAGGTAAAACCTGTCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT

GACTCCAAGAAGTGCATGTTCCAAGAACAAAGAACGGAGCAGTAGTACTGCCAAAAAATATAACAC
AACATATTTAAATGCTATCACTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAAG
TGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTTCTG
TGATTTATTCCCAATGAAGAGTTTATCAAATATTCCTTATGGTAATGACCTTTCCAACATTATTATC
TAATGGTGCTGGTAACAATTACACCAGAATCATTTGGTTCAGTGATTTTAAATTCTTCTTTAGAACT
TTTAAAGAGACTAAAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAAT
TTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCCC
TAACCCATACGTCCTATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAATG
TGGAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCGTGCCAATTCCAAAATGTGCTAC
TGGTCCAGGGTTCTCTTGTAAGCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATGT
TGACTTTGTTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATTA
TAAAATGTCACCTTACAATGCTCCTTTAGGTGATTTTAA

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVKLLNNGLLLAGQSVFQDVATPQQASVQQYNIVNSLGGSPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHERYPSKSNKSLAIIYAKFENYKGTFKGDLAFLNDYTYFVTDKNNYEKETSPKNSEGT
YAGTTNALRHGAARAKYGSLYKENSTLPVFSSNSGRYQTSRYFARGFLGDDFKEGKTVKFNIIS
EDADVANSITPRSACSKNKERSSTAKKYNTTYLNAITERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKYSYGNLDSNYISNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLLEIFHSALGLLEPAEDLPTSYIPFPNPHYVHSSIVPOGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVFVKQCGVNSTYPSSELTIFYWDYKNVTYNAPLGDF

YBR093C_homolog_4 1886bp PathoSeq: 1..102/1038..1062/1078..1886,
public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303)

ACTACTTAAATTGGCATATCCAAACAACTTGAAGTAGGAGTTTCCTTATTTTTATTTTGTATTTA
TATATTTGATTGCGATTAATGTCAATAATTTAGTTCCGTAATTATGTCACAAAAACAAACAATCA
ACATATTAAATCGTTATCCCAACTTTTGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGA
TGCACAATCAATTACTATAACTTTTTTTTGAACGTGGGCTCTGTTTAGTTTAACTTCTTGTAAGT
TTATTATTCGGATTGGGTAGCTCAATAACTGCATTTCTGTACAATAATGTTAATTCAATTCTAAAT
TCCGATGAACCGAACACACAAAAACATCCAGTTCTGGAGAGATTTTCAAACCTTCTATTATAAA
TAGAACCTTATAAGTCCATAATAATTCGAATTGAAGGATTATTTTCTTTTCCCTTTTCTGATTACTT
TCACCAATTTTCTTCTCTCCAAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA
ACGGGTTGTTATTAAGTAGTCAAAGTGTTTTCCAAGATTTGCTACTCCGCAACAAGCTTCTGTGC
ACAATATAATATACTCAATTTTCTTGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGA
TTTCTACTGATATCCCTGCTGGTGTGAAATTGCTCAAATTCAATTGTACTCAAGACATGGTGAAA
GATTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAATTTATGCTAAATTTAAAACTACAATG
GTACATTCAAAGGTGATTTGTCAATCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTAACT
ATGCTAAGGAAACTAGCCCCAAAAAATTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTC
ATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAACTCAACTTTACCAATCTTCA
CATCCAATCTAACAGAGTACATGAACTTCAAAGTATTTTCGCTAGAGGGTTTTTAGGTGATGATT
ATGAAGAAGGTAAAACTGTCAAAGTTTAAACATCATCTCTGAAGATGCTGATCTTGGTGCCAATAGTT
TGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAACTGAGCAGTAGTACTGCCAAAAAATATAACA
CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAA
GTGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTTCT
GTGATTTATTCACCAATGAAGAATTCATTAAGAACTCTTATGGTAATGATCTTTCCAAATATTATT
CTAATGGTGCTGGTAATAATTACACCAGAATCATTTGGTTCAGTGATTTTGAATTCATCCTTGGAAC
TTTTAAAAGACACCGAGAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAA
TTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTTCC
CTAACCCATACGTCCTATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAAT
GTGGAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCGTGCCAATTCCAAAATGTGCTA
CTGGTCCAGGGTTCTCTTGTAAGCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATG
TTGACTTTATTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATT
ATAAAAATGTCACCTTACAATGCTCCTTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSQVWL
SFAHDTDLLEIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVFIFKQCGVNSTYPSELTFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
TAATCTATGAACAAATTAAGAAGCTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA
TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAATAATC
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTCTCTCGCACATATTTTATTAGAGCTTAC
AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTTCGCACGC
TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA
AAAAATTATCAAAATTTTCAACCTTGAGAGAAAAAAGTGGAAAAAACTTCTTCTTACATTT
AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT
ATCAGTGATTATAATTAGAGTCTTTATTTGGATATTGCAATAATTGGATAATAAAGAAAGAGCATA
AGAGTAGGAGTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTATCGTCGTGATTA
TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAAATGAAGGACTAGTTTATTAGGGGT
GACATTTTGTAGACTACGTAAAAGTACTTTTCGATTCAAGGAAAACCAATTTTAGTATCTATCAACA
AACTACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTTAATCACTGAAAACAATAAACAT
GCAAACAAGCAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACAATACTTTTTTTTGTTCAT
TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA
AAATTACGTGTTTCTACGGAAAAAAGAATGGGTCAAGAAGTTGAAGGTGACTCAGTTGGAGATGAA
TTCAAAGGTTACTCTTCAAAATCACTGGTGGTACGATAAAACAAGGTGTCCCAATGAAACAAGGT
GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCCTTGTGTACAGACCAAGAAGA
ACTGGTGAAAGAAAAAGAAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTTGTGCTGTTTGGCT
TTGTCTATTGTTAAACAAGGTGACAATGAAATTGAAGGATTAAGTACACCACTGTTCCAAAAAGA
TTAGGTCCAAAGAGAGCTAACCAATTAGAAAATCTTTGGTTTAACTAAAGAAGATGATGTTAGA
GATTTTCGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAATTTACACCAAGCTCCAAAGATTCAA
AGATTAGTTACTCCACAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAAGTCAAGAATGCT
CAACAACAAAGAGATGCTGCTGCTGAATACGCTCAATTGTTGGCTAAGAGATTGCATGAAAGAAAA
GAAGAAAGAGCTGAAATTAAGAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
MKLNISYPANGTQKSMIDDDTKLRVSTEKRMGQVEGDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIVAQDLSVLALSIVKQGDNEIEGLTDTTVPKR
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTKGDKTYTKAPKIQRLVTPQTLQRKRALKAKKVNA
QQQRDAAEYAQLLAKRLHERKEERAIEIKKKRAESLKN

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAAACAAT
GATAACGGAGGAGGATTATCCCATACAAACAGAATAGTTGTTGGTGTAGTTGTTGGGTTGGTGGT
TCTATATTAATTTGTTGTTGGCCGTTTATTATTACTTGAGAAAGAGAAACAACCGTGATTATGAA
GGTGGATGGAGTTTCTGGAGAAAGAATGAGAAATTGGGAAGTGATGAGTTCTTCAATTGGTGAATTG
GGTGTCAGAGACAGAAATATTAATCAAGGATCAAATTTTTAAACAAGGCTTATTTTGGATGAGGGT
GGTTTTTTTTTATAAGTATTTTGTAGTTGAATTTAAAATTTTGTACCTTAAAGTCTTTTAATTTAAT
TTTAATAAAAAGTGGTGATTGTCGAACTTCAAGAGTATATTTGGTGAAAAAATTTTGTG
GAACTGAACGCGTCTAACATCTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT
TGAATGAAGATACAAACGCAACTAAATATACTTATAAATTAATACTACAGCTACCATCAAAGATACTAA
ATCAACTTGAATCCAAGTCAACTAACTTGTATATAAATCTGATATCAATTCCTTAGCATTATGCA
CTGATTACAGAACTTTCAAGTTACGACAAATGAACCATTCATAACAGTCTTGGCTATTGAACAAAG

AACCTGACAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG
GTTTCGATCGATACGTCCGATATCCCTATTTTCAACGGACAAACAGCACAGCAACCTATTGATTTGA
TAGCATTGGAAGATAATTCGATTTGTTTCACATCAAGAGTTTTTATCGAATTGGTATGAGTTGGGAG
GTTGTGAAATTGATAAATGGAGCATATATAATGAGTGCAGATATTATTACTGAACTATTATATCTAT
TAATCACCAAATTGATGAGTTTACAAGTGCACGAGTTTTCTCCGGAAGATGTTTCATCCATCATCA
CGCCCCCTTATAATGACTCAATGGTAACATCAATCATAACACAAATTTTGCACATAGAAAAGTGAGA
AATATCAATTGAATGATTTAAAAATTACACAGTGGTTTTGGCATTGTTGAGATGTCAAAAATCAATC
ATAAAATGACCGATATTTTCAGAGTCTTATTGAATTGGAAAAC TAGTTTGCCGTCATTCTATAACC
CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCCAATCGAAAACAAAATATTGTATG
TCGACCCAGAATCTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA
GTTTGGAACTATGATGAGTTTATTCCATTTCATTAAAAAGTTTGTTCCTGCCGGTAAAAAGGTGCGACT
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTTATAGTCTGTCCTAGAT
AA

YCL016C_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLROMNH
SNTVLLLNKEPDNKLIGFQKTSY EYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIITPPYNDMSMVT SII
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHMTDISEFLNWKTSLPSFYNPPLDISQLAGYYC
SPIENKILYVDPELSSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

GGTGGGGTTCCCATTTTAAATTTAAAAAAATTTTTTACCATCCAAAGGATTTTATTTACCCAAAGAC
CAAAAATTATTATTTGAAATGGGGATTAAATGGGGATAATTTTATTTTGCCTGATGAAAAGATT
AGTACCCGTTTGAAAGTCCTGATTCAAATTATGGTCAAGCTAAAAGAGAAATATTTGATTTAATTA
CTGGTGATAAAAAACCAAGAATTTTCCATGTTGATGAATCATTAATTGATGATTCTCAAGAAGCTG
CTGATGAATATGAAAAACAATTGATTAATAATTTTGCTAAAAAAGATTTCGGTGAAATTACCTTTAT
TTGATTTATTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTTCTAATCATGGTG
AACAATTGAGAGAAAAATTAGCTTGGGTTTTACCAGTATCAAATGCTCCTCTGGGACCAGAAAATA
GAATAACTTTATCTATCCCAGTTATATGTCAATCCGCAAGAGTGACATTTGTTGTTGAAGGGTTAA
CTAAGGCACCAATTATTAAACCATTATGGAAAGACCAGAAAAAGGTTTACCAAGTTCAATTGTTA
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTTGTTGATGATGATGCATTGAATGATTTGTTTGATA
TAATAAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGCPDGHIASLFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICH SARVTF
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSFVDDDALNDLFDITKKKYKYL SIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTCTGTTGGAGAGATAATTGAATTCAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATTCCCGGAACG
TCTTGGA CTACTTGGATACAACAATGGAAAAATGAGGAAAAATGAGGAAAAACGAGGAAA
ACGAGGAAAAATTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAGTGAACGCCCC
AAACAGAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAATTTTGGTTCAGAA
CACAACCTTGGGAAGAAAGAAAAAACCAGAAAAAGAAATTCATCTAAAACACATACACAATATAT
ATATATATATATAAATATATCCATATACATATGCTTTAATTTAACCTTCCCGCCTTTCTTTTCTTC
TTTTTTGAATTATATCGATTTTAAAAACTACACTTCATCATGGCTGGAGTTAGACAATTAAGAATAA
TAGCATTAAACGGCCTTTGTCTTGGTTTAAATTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTGGTTTCATGCACAAGCATCAGACCAACAACCAACATAACACCAAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTGATTCTAAAAATGATCCTCAAACCTGATGACA
AAATAAATCAAAAAATATCACAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACTAATAAAG
ACACCACCAAGTCAAACCAGATAATGGTGAATGATCCAAATATCTGATTTTGATAAAAATAGAT
CATTATCACC AATGACAATTTTCAGTAAATCATATTGTCCATATTCAAAAAAGATTAAACAATTGT

TATTAGAAAAATATGATATAACACCAGCACCAAATGTTGTTGAATTAGATCGATATGAATATGGAG
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAACTGTGCCAAACGTATTGGTTGGTA
AATCATTTGAAAGTAGGGGTGGTTGTGATGAATTTGAAAACTTCATAAAGATAATGATTTGATTA
AATTGTTAGTTGAATGGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAATACCCCATCAAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKDTNKDTTKVKPDNGEYDPIISDLIKIRSLSPMTIFSKSYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTVPNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVEWGSRLQVAKKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313)

AGTGGTTGTTCAATAATGGTAAGTTCTTGGAAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTTCAAAGTGCCTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCCAGTCAGTTAGTAGTGCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTAGTGAAAATGCGAAATATATCTGTACTGGGAACCCCCCGGAAAAAAAAAACCTA
TGCTCAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT
TAATATGGTGCGAAGAGCGTTTCCAATTTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTGTAGTAGAGAGTGCTCGCACTAACAGAACATTTTTTTTCAGAACAGGAAAAATTTTTGAAAT
CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAATACGAAAGGAAAGGCAATTTAA
AAAGGAAATCAAAAAGTCCCAACCTTGCAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC
AGAACGGTGTTACATAAATGGGATATAGAACAAAACCTATACGAGGAGTTTGTTCACGATCATTC
AATAACCAGAAAACGATAATATTTTAGCGACCATTAATGACACTTGAAGGCTCACTGGGCCAATA
GAATATCTCCATATACACTTTTGAACATTTTACTAACAATTTACTTTTGTCTTCTATGGCTTTGGTA
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTTAATTTAAATTAACGGTT
CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATTGACTTTGGTTG
GTTTAGATAAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG
TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG
CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTTAGTTGCCGACTCAA
GAAGAATGGAACCAAGAAATTCGGTGGTCTGGTGCCAGAGCAAGATTCCAAAAATCTTACCGTT
AA

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVEPLTLVGLDKFQGIDIRV
KVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEASKNELKKIFASYDKTLLVADSRMEPKKFGGRG
ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACCTTTGACAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT
CTTGAATACTTAAAATTCTGAACCTTGATCACCAGATCCTTTTCTTTTACATAATTAGATATGATGG
ATAGGTTAGAATCGTCTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGGAAAAG
TCACTCCACTGTATATATTTCTCGGAGTTTAAACGTACTACAGTTCAAGTGGGGTGAATACCTAAATAG
GGGGGTAGAATACGAACCTCTACAAATTTTAAAGGAGACTATGACCCGAAAAGAGAAGAAAAATTTA
TTACTCTAAGAACCTTTATATACCTCCACAACCTCACTTTTCTTTAGTTTCATTCTGCTTTTTTTTT
CTTACACATCTTAAAGGTCAAACAATTTAACTTATTAGCTTGTGAAAATCTCACTTCAATTCAAGTT
CTCTTTCAATTGACATTATAGTATTTCCCAATTCATTTATGGCTTCTCATGCTTCCTGTATATTCT
GTAAAATTATCAAAGGTGAAATTCCTTCTTTCAAGTTAATTGAACTGCAAAGACTTATTCTTCT
TGGACATTCAACCAATTGCTGAAGCCCACGTTTAAATTATCCCTAAACACCATGGGGCAAAGTTGC
ACAACATTCCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
AATTGGACGAAAATAATACTCCAGAAGGTGAAGGTTATAACGTTTACAGAACACGGAAGAATTG
CTCATCAAGTTGTTGATCACGTTCACTTCCATTTGATTCTTAAAAAGGATGAGGCTACAGGTTTAG

GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGATAAATTAGGAAAATTGCATGAGAAATTAAAGG
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)

MASHASCIFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNIPDDYLSDILP
VVKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
(SEQ ID NO 317)

CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT
GAGAGCCAGAGAAACCAACTGACTGAGTGATCGTCTCTCAACAATTTATTTCTCCTCGTCTTATT
TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTA
CCAAAACACTAGTATTTCAACATGAGAGATAAGTGGAGAAAAAGAGAGTTAGAAGATTAAAGAGA
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)
MRDKWRKKRVRLKRKRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:
501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)
TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAACTTATATTTGAAAGTAAATTCCTA
TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGTGGAA
TAAATTTAAATCCTTCTTATTGGTGTCTAGACTTTGCTTTTGTGGTGATTAGGGCTTTAGCCCT
ATCACGTGAAATACTGTATATAAAAAATTCTTTATAGCGCGATAAAACATATTTTTTTTCCGTATT
AACAAATATGTGTGAAGTTTTGTCTGGTGTCTTCTCACTGTTTTTCTTTTCTTTTCTGGTAGTAT
CAATTAACGCTTAGATCCAATACAGTTTTTGGTAACCTTGACACGAACAAAATCTCAAATTTGTTAC
TGTGTGAACCAACAAGGAAGAGAAAAAAAACCCATACAAAAATTTTTCAGTATCAAGGAATTAGA
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTAATATCGATATTATCCA
TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCTATTTAT
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA
ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTTTGGGTTTAGATTACTA
TATTTTACAAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTTCAGATTAGCCAAAT
AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCACAAATGAAACATTAATACTAATACTAA
CTTTTTTTTTTATTTATTAGGCCGGTGTATAAACTTTTGAATTAAGAACTAAATCTAAGGAACAATT
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAGTTCAAAAATTACAAAGACC
AAGTTTACCAAGAATTCACACTGTTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAAGTTGAA
TCAAAGAGAAAATGTTTCGTGCCTTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA
AAAGACTAGAGCTTTAAGAAGAAAATTGACTAAATTTGAAGCTTCTCAAGAAACTGAAAAAGCTAG
AAAACAAAGAATTGCTTTTCCACAAAGAAAATTTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)

MAGVKTFELRTKSKEQLESQVLVELKQELATLKVQKLQRPSPRIHTVRKNIARVLTVINLNQRENV
RAFYAGKKYIPKDLRAKKTRALRRKLTKFEASQETEKARKQRIAFPQRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
501..2687 (SEQ ID NO 321)

CTCTGTGTAAATTGATGAAATCCACACAATAAAAAATTTCTTTCTTTCTTTTAAAGAACCTAAAAACA
GAATCAACATTATTTGCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAAATAGA
AGAGAATCAAACCTTAACATTACTGTTACGCAACGTCAAGAGGGCATTTTTTTTAGTTTTAATTTGT
TTCATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACCTTTCTTTTGTATTTTATCAGGGAA
GCCACATCCAACCACAGTTACATCCCAACAAAATCCCTTAATCTTGTCTTAGTTGTATTATTAAT
CTATTGAATTTAAGTTTGATATGCGAGAGAAATATTGTGGATTGTATAAGTTTTGAAGTGGACTGTA
ATACTTTGAGGGCTTAATCATATATTGACATTTTATACCTTACTCGCGGTGTGCTTACCACACTG
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTATGAGTGATATTTATATTATTATTCATA

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCACTAAGGATTCTTCCGAGTTAATTGAATTTG
CTTGGGAAACAGTCGATAGTGTCACTTTGGAACTTTATACAAAGGATCAAACCTTGGTTCGTCCAA
CCAACACACCTATCACACCTTACTGCTCGAAGATTATAGATAACATGGGACAATGTCAAAAATG
CTGGGTCTGTTCAAAGACGCCATCACAACTTTGATCAATACGTACAAGAACACATAAATTTCCAAGA
AAAAGGAGTTTTCAATTGTGATGTTTGACATTTCCAAATTGAGAGTTCAGTTGGTTCGTGAAGCTA
GAGACAAATCCGTGGTTTTACCCTCGTATCTACAACATCCAAGGATTTTGTATTTACCAAGAGAAT
ATTTAAATTGGCAATCTAGCCACCCTGAAACATTATCATACCCCCCAACTTCTTTAACTAATATTA
TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTCGACTTGCCAACTTTTCTTCCA
CACCATCACCATCAAAGCTTCAGCAACAACGACGACGACAACTGCAAATGTCACAGCCATTGACG
TCCTTTCCAGTGAAACAGAACCAATGGTAAAGTCATTGCAAATTTGCACGCCAAAATTGCCAAAC
AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCCCTAATGTATTTACAAGACCTTTTGATTCCG
CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAAGTACTCTATCTTTCCAACCTTGCCAAACG
ACACCACACAATCAGAGTTGGAATCATGGTTCACTCAGTATGGTGGAAGACCAGGTGGGTTTTGGA
CTTTTAAGTCTGCAGATGATAACAATAATAACAACAACAATAGCAATGGCGGGAAAGGATATC
AGAATGCGAGAAAATATGGTATTTTCAAGGTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT
GTTTAGCTTTGAATGGGAGAGTGTGAAATGATCGTCCTATTGAAGTTCAAGCGTCTTCTAGTAAAG
TGTTTGATATGGCCATGGATAAATTGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC
CCGGGGATTGGCAATTGTTTATCTTGTGGGTTTTCCAATTTCCAGAGAAGAACACACTGTTTCAAGT
GCTCTTTTGGCGCAGTGGCGTTTCAGGATGTTTTTAACAGTAATACAGGCAATACGCCAACGGTAATG
GCAATGTTAGCGGCAACCACAACCACAACCAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC
CTGCTCAAGCTAATGAGAAAATTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA
AGGGTCCAACAGGTAATGTCACTAATCACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA
ATCTTAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCACAACAACAATA
ATAACAATCATGGGAATAGCAATGGTAACACCATACATGGTCGTTCCCAATTATAACAATAGTGTTT
CATTTAGAGCAGGTGACTGGAAATGTGAAAATTGCATGTATCACAATTTCCGCAAAAATTTGTGTT
GTTTAAAATGTGGTTCGCCAAACCTGCTATTAAACAATCAACAAAATAATAAATTCATTCGGTGA
ATTCAACGGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAACTTGAATAATAATG
CATTTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC
ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCAAAGAATCAGT
ATTACAATAATAATAGCAAGAACTCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC
AAAATCAAATTTTGATGTATTCACAACAATTGCAACAACAACAGCAACAACAACAGCAACAACAGC
AACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIHISTTCDDSPFVTKDSSELIEFAWETVDSVTLETLYKGSNLVRPTNTPITPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHIIISKKEFSIVMFDISKLRVQLVREARDKSVVLPSYLQH
PRIFDLPREYLNWQSSHPETLSYPPTSLTNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTADVLSSSETEPNGKVIANLHAKIAKQLIKKSIPVENHPNVFTRPFDSAQDITAFTERS
VLYLSNLPNDTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNNSNGGKGYQNARKYGISGFVA
FNTHEEAVDCLALNGRVLNDRPIEVQASSSKVFDMAKLLLTSPFLSKNRPRPGDWTCLSCGFSN
FQRRTHCFRCSFAAVAFQDVFNSTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGN
SIPSyndPIKGPTGNVTNHLNSETNLSNNTNLNNNNHHNNYHNNYHHNNNNNNHNGNSNGNTIH
GRSHYNNVFPFRAGDWKCENCMYHNFKNLCLCKGVAKPAINNQNNNTIHSVNSTAAIAAATAS
GQPLNLNNNAFLNLQQQQSQSQPOGQHYNQHSRNNNASGASKFNNGYNPKNQYYNNNSKNLSNNF
GLNGMHQONQNIILMYSQQLOQQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDNLNGSSSSSHQSKLQL
NNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,

PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

AATAGCATTGAACAAGAAGAAGAGGACAACGATAGACCAAGGTTGGTTTTAGCCAATCCTGATTAT
GATAGTGATGACAGTTCATAGACAATTTACAGCCTTAAATGGATATATATGTATATTTAATAATAA
AGGACTTGTTTTTTTTTAGTAAGTGTGATCTCTTTTCTGGGTGTACATTTCCGATAGCCAACCA
GGTTATATTTAGCAGTTTATAGACAGTGTATTCATGATGGGTAATATAAATAAAAGCTCAATGAATA
CTATCTAGTGATAAAGTCGTGTGTAATCGATTTGAAAAATATAAAACCATAACGTAATGAAATG
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAATGTTGTCCGCCAAAAAAG

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTGTGTCACCATAACTATCAATTGTTCA
CCTCTTGAACCAACATCAAATTGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG
ATGATGTGAAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAAATGGAGACCCCTTACCTG
ACTTGTGTGATGCATATAATCAGATTTGTGCATGCCTTCCAGAAATAAAGAATTTGAAAAAGTTGTTGT
ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAATGAGACATGAAATGATTCTTG
TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTTCGAGGCAATACTTTGAGAT
ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAACCTTTAGTTCCTAATGTCCGTCAATGTTTAG
AACACCGTCATGCCTATGTGAGAAAAATGCTGTTTTTCGCATTATGGTCTATTCATAAAGTCAGTG
ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTGTATGAGGAAAAACGATTCTGTTT
GTAAAAGAAATGCTTTTGTCTTGGAGACTTTGAATAGAGAAGCTGCTTTGCAATATATTACAGG
ATAATATTTTCAGTTATTGAGACTTTGGACTTCATTGATACAATTGGCTTTTATTGAGTTTATCAAAA
AGGACTCTATTCAAAATCCAGCTTTAAAGCAACAATATGCCCAATTAATGACAGAAATTATTGAAA
GCTCTTCAAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT
CAATTTTGTGGCAGGAAACAAGTTTGTGTAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA
TTATCACTTTAGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTTACAAGACTTGTCAT
TAGAAATTTTACGAGGTTTATCTTCCCAAGATTTGGATGTTAAAAAGAAAGCTCTTGATGTTACTT
TACAATTTATCACCACCAGAAATGTTGAAGATGTTGTTAAGTTATTGAAGAAAGAATTGCAGTCTA
CAGCTTTATCCAATGATGACAAGAATGCAGATTATAGACAGTTGTTAATTAATGCCATCCATCAAT
TGGCTATTTAAATTTGTGGAGGTTGCTGCCAATGTCTATTGATTTATTGTTGGATTCTATAGCCGATT
TGAATACCACTGCCGCCACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATTTCCAGATT
TAAGGGACGCTATTTTGAAGAAGATTGATTTTGGCTTTGCCACATGTGAAAAGTGGTAAAGTTTCC
GTGGTGCATTATGGGTTATTGGTGAAGTATGCCCTTAGAGGAATCATTAAATACAAGAATCTTGAAAT
ATATTAGAGGAAGTATTGGTGAAGTACCAATTATTGCTAGTGAATTGAAACTGAAAAAGCGTGATG
ATACTGAGGAATCACAAGAGGAAGAAACCGAGTATGATGGTAAACCTCGCAGAAAGGGTCCAGTTG
TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTTGACAAGCGAAACAACACTGACTCTTTGAAA
GTGACAGCAAGACTCCTATCAGAAAGCAAAATCTTGTGCTGATTCTACTTAGTGCTGTATTAG
CATCAACTTTGGTGAAATTGATTCTCCGATTGCAAAGTTTGAACAAACTCAAGAAAAAATTTTGA
ACGGATTAAAAGCAGAAGCATTGTTGATTATGGTTTTCGATTTTAAAGAGTTGGGGAATCTAGCTTGG
TTTCTAAGAAAATTGATGAGGATTCTGCTGACAGAATTTTGTCTTACATCAAGATTTTGAACGATG
AAGAAGACCTTCAGGAAATCAAGACAAGCTTCCTTGAAGATACTAAAGATGCATTTAAAGCACAAA
TTAATAATGCTGAATTGAAGAAAGCAGAAGCATTGGCTAAGGATTTGCATGATAACGCTGAACAAA
TTGACGATGCAATTGTTTTTAGACAGTTGGATAAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG
ATGTTGCTGCTGCGTCAGGAAGCAATGAATTAAAGAAAAGAAATTTGTCGTCGAGTGTGAACAAA
TTATACAATTGACTGGGTTTTCCGATCCTATTTACGCAGAGGCATTTGTCAAAGTTCATCAATACG
ATGTTGTGTTAGATGTCTTGCTAGTGAATCAAACCACAACACTACTTTAAGAACTTATCAGTTGAAT
TTGCTACATTGGGTGATTTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT
TCTACAAAGTTCAAACAACATTTAAAGTTACTTCGGCTGATACTGGTGTCATCTTTGGTAACATAG
TGTATGACGGTCAACACTCGGACGATTACGTATAGTTATTTTGAATGACGTTACGTTGACATTA
TGGATTACATTAAGCCAGCCACTTGTTTCAAGAAAGTCAATTCGGTAAATGTGGAACGAATTTGAAT
GGGAGAATAAGATAACCATTAATACCTATTGAAACATTGAAAGAGTACTTGATGAATTAATGA
AGGGTACAAATATGCAATGCTTGACACCGGGTGCGGTAATTGGAGAAGAATGTCAATTTTTATCAG
CAAACCTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA
GTGATGGACCAATAATTGGTCATGTGAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTGCTATTGG
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSVNEFKNLLEKGDVVKVDTMKKILITILNGDPLPDLLMHIIIRFVMP
RNKELKKLLYHYWEVCPKMDSESGMRHEMILVCNAIQRDLOHPNEYIRGNTLRYLTKLKEPELLET
LVPNVRQCLEHRHAYVRKNAVFALWSIHKVS DHLPDADELIYRFLYEENDSVCKRNAFVCLGDLN
REAAQYIQDNISVIETLDPLIQLAFIEFIKKDSIQNPALKQQAQLMTEIISSSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRESNNDVKIITLERINQLHKQHPGVLQDLSLEILRGLSSQDL
VKKKALDVTLOFITTRNVEDVVKLLKKELOSTALSNDKNADYRQLLINAIHQLAIKFVEVAANVI
DLLLDSIADLNTTAAAYEVITFVKEVVEKFPDLRDAILRLILALPHVKS GKVFRGALWVIGEYALE
ESLIQESWKYIRGSIQEVPIIASSELKSKKRDLDEESQEETEDYDGKPRRKGPVFLPDGTYATESAL
TSETTDSLES DSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQTQEKILNGLKAEALLIMVS

112/161

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAEALA
KDLHDNAEQIDDAIVFRQLDKDNKSKASVDDVAAAAGSNELKKENLSSRLNKIIQLTGFSDPIYA
EAFVKVHQYDVVLVDVLLVNQTTTTLRNLSVEFATLGDLKVVDKPTTANIGPHGFYKVQTTIKVTS
DTGVIFGNIVYDQHSDDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNEFEWENKITIKSPIET
LKEYLDELKMGTMQCLTPGAVIGECCFLSANLYSRSSFGEALANLCIEKQSDGPIIGHVRIRS
KGQGLALSLGDRVASISRK GK KATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
CDS: 501..2267 (SEQ ID NO 325)

GTTTGATCACATGTGTTGTGAACACTCGGGTAATACAAAATAGTGAGAGAGAAGAAGGGGAAAAAA
AAAAGCAGAACACAAAACATGGAATTTGAAAACAATTTTGTAATTCAATCGATCCGAGACTTCCAT
AGCAAAGTTAACAAGCACAAATTGTCATTTTAACTTAATTGGTGGATTAATCGGGATCAATCTGAAT
TGTTCCTCCGTATTGTTTAAAACCAAAGAAAAAGGATAATCAAACTAAATCTTTCATATTAACACT
ACCATTTTGTAGTGGTCAGTTTATATAATTATCCACTGTTCTCTTCACAATTAACAAAAA
AAAGAAAAAAGAAAGCTCTCTCTCCCCAAAAGAAAAAGCAAAGGTAATTCCTTCATACACACCTT
TGATATCTTTCCTCTTAGACTTTTCTTTTAATACTTGCATCAATTGGAATATTACTTGTTCATACT
GGAGTTTTTCATTGAATAAATATTATTAATAATATTATTATGCTTGAATTGAATTCAATTACGATTC
CTCGGAATTTCACTGAATTCCAACTCACAGCATTAAGATCTACTATCAACTTAAGATTTTATTTT
TTGCCACACTACTGTGCTCAAGGATCAATTTGGCTTGAACGGTTCACTGTTTGTAGCAAGAGATATTT
TTGTTGGCTATGTTGTATACACTCAATTATTAAAGCTTTATCGAGTATTAAGAGGGTACGGTATTG
TAGATTCTATTGCAAGGTTATACCTATATGTTAGTTCTACGGTGTCTCAATCTTTTCACTAC
CATTTATTAAATCCAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA
TGAAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG
TTTCCTTGGAGTTGGATAAAATTACAAAACCTGAAACATTCTGACTGGATCAATGGAAGAGTCAGTG
GAGCAGTTTATCATGGAGGTGAGAATCTATTGTCATTACAAGTTGAAGCTTACAAGAAATACTCGG
TGGCCAAATCAATTCATCCCGATGTTTTCAGGTGTCGTAAGATGGAGGCCGAAGTAGTTCATA
TGTTTTGGATATCTTTAATGCTCCGAGTGACGGTGTGGATCGACAACCTTCGGGAGGTACTGAGT
CGTTATTGTTAGCCGGTGTGTCAGCTAGAGAATATGGGAAGAAATATCGTGGAAATAACTGAGCCTG
AAGTCATTGCCCCCGTGACAATACATGCGGGAATTGAAAAAGCCTGTTTTTATTTTGAATGAAAT
TACATAAAGTTGACTTAGATCCGGTTACCTTTCAAGTTGACGTTAAGAAAGTAGAAAGATTGATCA
ATAGTAATACAGTTTTAATCTGTGGATCAGCCCCAAATTATCCTCATGGAATAATTGATGATATAG
AGTCCTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCAGTTGATGCATGTTTGGGGTCAT
TTATTGTTTCGTTTTTAGAAAAATCAAAAGTACATGGCGATAGGAAATTGCCCATATTTGATTTTC
GATTACCAGGTGTCACGTCAATCTCATGTGATCTACAAATATGGGTTTGCTCCCAAGGGGTCAT
CAATAATTATGTACCGTTCGCCAAAATTACGTGAGTGTCAATACTATATTGCAAGTGATTGGACGG
GTGGAATGTATGTTTCTCCAACCTTTGGCTGGTTCCTAGGCCAGGTGCTCTTGTAGTTGGATGCTGGG
CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTGTGTACGATATTGTGCTGGCGTCAA
TGAAAGTTAAACGAGCAATTGAACTGACCCGATACTATCCAAACATTTACAAATTATTGGTGATC
CAATTGGGTTCGGTAATTTTCGTTTCAACTTGCACCTCAGCAATCGGGAAATTAAAGTATTACGAGA
TTAGTGATTTGTTGACCAAAAAGGTTGGCATTTTGCAACTTTACAAAACCCATCAGCATTACATT
TTGCATTTACAAGATTGACTGTCCCGGTGGTTCGATGAATTGATTGCAGATTTGGTTGAAGCTACAA
AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAGAATGGAGTGACCAAAGCTCCAGGTGATACTG
CTGCGTTATATGGTATAGCTGGCAGTGATACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT
TTTTAGATACCTTATACAAAATTGTA

YDR294C_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGIVVYTQLLKL
YRVLRGYGIVDSIRRLYLVSSTVSSQIFSLPFIKSKIDKELQATIGKVEEIMKNDPQLLQFPEL
PEQGIDADNVSLDKLQNLKHSWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVPFPGV
RKMEAENVHMLDIFNAPSDGCGSTTSGGTESLLLAGLSAREYGKKYRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSFIVSFLEKSKVHGDRKLPFI FDFRLPGVTSISCDTHKYGFAPKGSSIIMYRSPKLREC
QYYIASDWTGMYGSPTLAGSRPGALVVGWCWATLINIGKQGYTKFCYDIVSASMVKVRAIETDPIL
SKHLQIIGDPIGSVISFQLAPQQSGNLSIYEISDLLTKKGWHFATLQNPALHFAFTRLTPVPVDE
LIADLVEATKEAVAIAEEHKKNGVTKAPGDTAALYGIAGSVHTAGLADRLIVAFDLTLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public:
331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)
TTCAATTTTTTTTAAATAAGTATAGCAAAAAGGTATTTCTTAGAAATTGAAAAAATCACAATAA
AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATACAAATGAAATGA
TTCACATGAAATATGTTACAATTCCACACTTGCTGCTAAAAAGCAACAGTTTTTGCAATAGAGAAAA
GCATGATATACTATCGATAATATCTTTTCGATAAGAACTTAAATGTAGCAACGTTGAATTTTTAAAT
AAAACCTTCCTTTTCTGCTGATAAATTTTGACTTTGAAGCATAAAGAAGACAGAGCTAAAAA
CTACTCTCTAGACAAAATCAAAACCTCGAATATATTTTTGGTGTTTCTTTTTTTTTTTTGCCT
CTCGTTGAAATCATCTCCATTCTTCTTTTCCACGCTCTTTGTTGAAAACCTTTGCAACCTAAAAAAT
AAGAATCACTCCAACAAGTTTAAACTACATTATCAATTATGTTGAAAACCTAGATTAACAACAAGCA
GGCCATAAGTCGGGTTGTAAGAAGATATGCATGCTCACACCCCATTTCTCCCAATCTTGATAAGT
ACCCAGTTGGTCTAAAATGTCATGGTTACGAAGTTACCCAAACATCACCTATCCCAAGATTTTCCC
TCACTGCTGTATCATTAACAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCTAATG
ACAGTAATAATGTATTTCTGATTGCCCTTCAAAACAAATCCTCCAGATAATACTGGGGTTCCCCATA
TTTTAGAACATACAACCTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTTTAAATGA
CCAACAGGTCGTTGAGTAACCTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG
CTACCACCAATTCAAAGGATTTTGAAAACCTAATGGATGTGTATTTATCGTCAGTGTGTAACCGC
AATTAACCATACCGATTCTTGAAGAAGGATGGAGAATAGAAAATCAAAATGTTTCATGACATAT
CGTCCAAGCTTTGAATTCAGGGAGTTGTATATAATGAAATGAAGGCCAGTATTCGAACCTTGCAT
ACTACTTTTATATCAAGTTCCTTGAGAGTATATATCCATCCTTGAATAATTCAGGGGGTGATCCCA
AGAAAATTGTTGATTTGCTGTACGAGGGTTTACTAGAGTTTACCTGAAAAATTATCATCCATCAA
ATGCAAAAACATTTACTTATGGAAAATTACCATTGGAAGACAGTTTAAAGTAAATAAGCAAATACT
ATGAATCATTCGAAAAAAGGTGTCTTCAGTTGACGTCAAAACACCTATATTTTCTACAGATAAAT
CAGAAATCTTTGATGTCACCATCCCGGGTCCAGTTGATACAATGAATGGTAAAGAGACTTCAGAAC
AGTAATGCACATCTATCACCTGGAACCTGGGTAATCCATTGGATCCAAACATGCAGTATGATATTT
TTAAATGGAAAAATTTGAGCTCATTATGTATTTGATGGACACAACCTCTCTTTCTATCAAGAGTTAA
TTGAAAGTGGAATACGGTGACGATTTTTCTGCAAACTACTGGGTTGGACTCAACCACCGCGTTGCTTT
CGTTTACTGTTGGTCTCAACTACTTAACCAAGCAAAAAGTTGATAATTTAATGAAAAAGTTATGG
AAATCATTAATAATAAAATCATTTCCCGAATTAAGTAACGAAGAGTCCTCTTCATATCATGGTAGAA
TTGATGCTATATTGCATCAAATAGAAATAGGATTCAAAGACACAAGCCCGATTTTGGATTTGGAT
TATTGAGCTCTATTGTTCCGTCATGGGTGAATGGAGTTGATCCAATTGACACCTTGCAAGTGGA
AGATATTGTCGATTTTAAAGAAGATTATAAACAATAAGGTTTAAAGGATCTTTAAAGAATTATTAG
AAAAGACATTGTGTAACCTTCATTTCGCAAAAATTTAAATTCACCATGGAGCCAAAGATTTTAA
CCAACAATTGGTAAAAGATGAGAATTTGATGATCGAGAAAAGAGTAAGTGAACCTCACAGAAGATA
ACAAGAAGGCAATCTATGAGCAAACTTGGAATTAGCTAAATTACAATTGGAGGATCAAAATACAG
AAGTTTTACCCACATTGACTATTGATGACATTCCAAAGAGAGGTGATTTTTATGCCATTGATTTGG
GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG
CTTTAAAGATATTTCTATTTACCCACCAAACTTTACAAGTACCTTCCATTGTTTAACAACTGTT
TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAACTAAATAACAAATGTTAA
CTGGCGGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
AGTATGTGTTAAGTGGAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGTTTGGAGA
TTTTAACTACTACCAAATTCGACACCAGTGATGAGGTATTAGAAAAGTTGTCAGTTTTGATTA
ACATGGGACAAAACCAATCAATAATATTGCTGATCGCGGTCAATCTTATGCGGCTGCTGTGAGCT
CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG
TAATGGAGTTGAACTCCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCGGA
TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAATCAAG
AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAAATTTGATAAGGATATTTCTTCGAACAGACCAA
CTTTATCGTTAACAGTAACAGATGGTTTACTGGCATTTGTTGAACCTCAATTCAATTACAATCATA
GTGAAAATGTCTTAGTTAACTTACCATTTCAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT
CGTATTCATCAAAGGATGGTGCTTCTTACAAATATTATCTCAGTTATATTCCTTTAAAAATCTAC
ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTTGAACGGGA
CATTAACCTTTTATTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACCTTTAGAGATTCTT
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTCC
AAAGCGTCGATGCTCCAATTAATATCTTCTCAGGGTGCTAGTGCCTTCTTTGAAAATATAGATG
ATTACTTGAGACAGGAAAGAAGAGAAAACTTTTTGGGTACCACTTTAAAGGATCTCAGAGATGTGA

CTGAAAAGTATCTTGTTGATAACCAAAACAACCTTGTCACCTGTTATTGGTGACAATGAAATTTTAA
ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSRASRVVRRYACSHPISPNLDKYPVGLKLHGVEVTQTSPPIPEFSLTAVSLKHTESGA
THLHLDSPNDSNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT
GHDYTFYFPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE
MKGQYSNSAYFYFIKFLESYPSLNNSGGDPKKIVDLSYEGLLFHSKNYHPSNAKTFTYGKLPLE
DSLISKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCTSIITWNLGNP
LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNYLTKQK
VDNFNEKVMETINNKIIPELSNEESSSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWVNGV
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKLCNPHISQKFKFTMEPRDFTKQLVKDENLMIE
KRVSELTEDNKKAIYEQNLELAKLQLEDQNTLEVTPLTIDDI PKRGDFY AIDLGQVNNKVVHERVV
DTNGLVYANALKDISYLP TKLYKYLPLFNNCLTNLAGTENTPITELETQIOMLTGGITFSSKISTD
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILT TTKFDTSDDEVLEKLSVLIKNMGNQINNIADR
GHSYAAAVSSSKLTPSKYISDIVSGLSQVQFVMEINLSKLESEGKEYLAKEIIPILQEIQKYVLQGE
FRYRLVGNQEIIVENEKLIEKFDKDISSNRPTLSLTVTDGLSALLNSFNYNHTSENVLVNLPFQVG
YSSLGKIGSSSYSSKDGASLQILSQLYSFKNLHSKIRESNGAYGGGLTYDGLNGTLNFYSYRDPNPV
KSIQTFRDSLSYGLDANWNDKDLQEA KLRVFSVDAPINISSQGASAFFENIDDYLRQERRENFLG
TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVDNWKQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548,
intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TTAAGAACTAGCAGATGTAAATGTTTTATGTCATTATATAATTTGTTAATACATGTATATAGATT
TTTTAATGAATGTATTCCCTAAATAGAACAGAATTATGATGCTGTTACAGCAAAAACCTGGTTTGAG
TATTGGAGAAATGTTATAAACTGAAATTTGATTACAACCAAAACCCGTGTCACGTGTAAGTAATTA
GGGCTTTT TAGGGCTTTCTATATACAGGCACCAAGAAATTTTTTTTATGGGCGATAGAAATAATGTAT
GCGCGCGATTCTTCTCTGCTAGAGGTTTTTCTTTTTGTATGTCTGTAAACAGTGC GACTCACATAGTT
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCCCTAATCACATAGTTAATTTCTCAA
CTTTCTCTCTTTCTCTCTTTGCTTTTCTCCTAAGGAAAAAAAATTTATTTTCATTTGTTGAAAAT
TTTTGTATAGTTTCAGTTTAAACAACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAAAGGTT
CATTTCCAACACATTTTACGGTATGTGAGTGATTATAAGATTATTTGAATGAGATAGAAAAGGGTT
AAGGAAGGAAAGAAATTATCCAACACTGTTTTGGGAAAGATTAAATCAGAAATTTGAATGCAATGA
AAAAACTTTTTTCAAGAGATGGATATGGAACAAGATTCTGATTGTATCAACAAATATAAAGAAAAGC
AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG
AGTAATATGTTTTCAATATTATCAGAGACTTATCAAAATTTATGAGTTTATTATTATTGAAGTTCA
ATACCATCAAGCCTTTTTTTTAAACCATCACTCTATTCAACAATCATTATAAATATTAAAGTCTTTTT
TTTCCCTGTTTAAAGTATTCGATTTACTAACATTATGAATTATTATTATAGTTTGTAAACACCAA
CATTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC
CAACTTGGTTTGTAAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA
ATTGGAAGAAGATTGTCACCAATTATGCAAAACCCAACCAACTATAAAATCCCAGCTTGGTTCTTGAA
CAGACAAAAAGATCAAGTTGATGGTAAAGATTACCATGTTTTAGCTAACAACTTGAATCTAAATT
GAGAGATGATTGGAAGAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT
GAAAGTTAGAGGTCAACATACTAAACTACTTCTCGTGGTTCGTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)

MPLVVQEQQSFQHILRLNLTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKLRDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1:

501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)

ATAGTTATTACAATATAATAAAGCAAATAAATAAAGAAATGATAAAGAACCATATTAACAAAGTT
TGAACGTGCTGTAAGTAAATCTTGATACGAGAAATATTCATCTTGGAATATTTCTAAACGATACTG
GTAATACCTAATTTCTATTTGGTGTGGTACCTGCTAGGGCTATAGCCCTAATAGTATATATGCA
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT

115/161

TTTTCACACTAAGTTAAGGAGAGTGCAGAAAAATTTAGTACTAACAAAATTTGTATTGTGTTGTGTGT
GGCTATTGGGCAGAGCGAAAAATTTACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACACAC
AAACTCTGTGCGCAAGAAGAAAGACAAAAATTTTTTTGAAAAAAAAAAAAAGAGACAACCAACCTT
TTATTGTATTAAACATTTTAAGATATCAAGAACTAAAAATGGCTAAGTTCATCAAATCTGGTAAAG
TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACATGAATGG
GATAGATATATATGATATGGGAGAGAATTTTGAAGGATTGAAATATTTTATATAAAAAGAGAGAAGC
AAAGAGAAATAATGAACAATTGAAAAGAAGATACAAATACTGTTAATTAACTAGAAATATGCCATT
GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGAATTTGGGAGATTCTTTTGGAGTTAAGA
AAAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAAGACATCAACGAATCCCACAACATTT
TTATTTATTCATATCCATCATATGGCAGTAACAATCATGAATCTACAAATTACATTTAAAAAAGC
ATTATACTAACTAAATTTTTTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAGTAGTCAT
TGTGAAACCACATGATGAAGGTACCAAAATCTCACCATTCCCACATGCCATTGTTGCTGGTATTGA
AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACTAAAGTCAA
GCCATTTGTTAAATTAGTAACTACAACCATTTAATGCCAACTAGATACTCATTAGATGTTGAATC
ATTCAAATCTGCTGTCACTTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT
TGTCAAGAAGGCTTTTGAAGAAAACATCAAGCTGGTAAGAACAAATGTTCTTCCAAAAATTACA
CTTTTAA

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)

MAKFIKSGKVAIVVRGRYAGKKVVIVKPHDEGTSKSHFPFHAIVAGIERAPLKVTKKMDAKKVTKRT
KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKAFEEKHQAGKNKWWFFQ
KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

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CTTTCGTGATTGCGAAAGCCCCAAAATGTTTCGTTTAAACAACGCACACACATGTGAAACCTAAACCG
AGTTAGTCGTCAAGAAAATAATTCAGTGTAAAGTCTGTACCTTAAGCGTCAAACGTACTTCTGCA
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAACCTACAAGCTACGAAAAA
GAAAAAGAAAAATAGTACGAGTTCTTGGTGAGATAAATAATGGAGAACACTTTTTTTTTTCTCTTT
GGAGGTTTTAGAAGGCCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA
CTGCGCCCAAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG
TTAAATTAAGCAAGATCAACTCGGAATTATCCACATACCAACAAAAGATAAGCAGAATGAGAGACG
GACCCGGGAAGTCGGCACTAAAACAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG
CTCAAAGGATCAGTTAGAGAATCAATCTTGGAAATATGACACAAGCTTCCATGACAACAGATAACT
TACAAAATACCATGGTCACAATAAATGCAATGAAAACAGCCAATAAACTGTTGAAACAACTTATG
GAAAAATTAATATCGATGAATTGGAAGATCTTCAAGATGAAATGTTGGATTTGATTGATAAATCAA
ATGAACTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATTGATTTTGAATGAAATGGCAGAGAGTGGGATAG
GTGCACCTAGTTACTTAAATGATACAGAACCTACAGCAGCAGATAAATTGCCTACATTTATTGACG
AACAACCAGAAGAAGCTCAAAAAATCGCAAACTAG

YDR486C_homolog 218aa (SEQ ID NO 334)

MNRLFGTKSTAPKPSLNDAIKGIDERVGSLDVKLSKINSELSTYQQKISRMRDGP GKSALKQKA
LLRQRKQIEAQKDQLENQSWNMTQASMTTDLNLTQNTMVNTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSLEALSTSYDVPDDISESELDAELEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEQPEEAQKIAN

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS: 501..4547 (SEQ ID NO 335)

GAATGAGATTTTTTTTTTTACTAAGGGTGCACTACTACTAGTTATTTGTTTTTGTGTTGACGATCA
TTAAAGAAAAAATTTACAGTATACACAAAACACTTTACTTCTGCTGTTTTTTTTTTTATTATTAGTTT
TTGGTTTTCATAAATTATTAAAAGAAAGCAAATAATTATTGAAATAAATTTTATATTTTTTGGTTTTT
TTTTCTTTGGTTTCTTTGAATTTTGCAAACCAATCCAAATTTTTTTTTGAAAATTTTTCTTCTTCT

TCATTTGTTGACTTTTGAAGTTTTATTCATCCATATTCTTCAAGTTAAAATAGTGTTCAATATCT
GTCCAACCAAGAAGAAAACCAATAAACACATCAATTCCAACTTGTTTACATCAAACAGAAACAA
AAAACAGATAATTTATAGACACCTTCATTCATTTCGTTATTTTTTCCAAGTACTACACGTCCTTTAT
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CGTCATCGATTATGTCCCAATCAAATCATATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA
AAACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACACTGGTCAAAAAG
CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT
TACCATATGGTATAGAAAGAGAAATTATTATAATGAAATTATTAACTCATCCTAATGTTTGGAGAT
TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTCTAGAAATACGTTGAAGGTGGAGAAT
TATTTGATTTATTGGTGGAACGTTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAA
TCATATTGGGTACGGCTTATTGTCTATGCTCTTGGTATATGTACAGAGATTTAAAACAGAGAATT
TGTTACTAGATTCTCAATTGAATGTAAATTAGCCGATTTTGAATGGCAGCTTTAGAAAGTAACG
GCAATTTAGAGACTTCTTGTGGTTCACCTCATTTATGCTGCTCCAGAAATCGTTAGTGGATTGA
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GATTACCCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA
TGCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAAATGTTAGAGGTTGATCCTA
TGAGAAGAATATCTACTGAAAAATCTTAAGACACCCATTGTTAACCAATACCCAATGTCAAACG
AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA
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AATCCCCAACTAAATCTCCTTACGGAAGAAGATCAAATTCACAAAGACAATTTGAAAATGAACCAT
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CATCGCTTCCACCTTCTTACCTTCAAAAGATTCTCGTTATATGATCGATGAACCCAATCAACCCC
AGTTGCAACAACCTGCTTTAAGTCAAGTCCCTGAAAATCCTATTGTTGATGAATCCCCTGATTTAA
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CCAAAACTTGACCGCTTTAAGAGCATTATCTGAAGGAAATCATGCATCTGAAGAATTGACATTGG
AAGACGTTGAGAATTTGAAGAGACGATCAGCATCACAGCCGGTTCCAAAAGAGACAAACTCCGG
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GTAAAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTGTTGAAGAGGACCAAGGCC
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ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAGAAAATCTGAACCCAAGACTCTTATTA
GCAATGTTCAAATACCGAGTGTACTAGAAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT
CGGTATTGCTATGTATTCAACAAAGGAATCATACCGTGAATTTGAATTTCTATAATTAACCTCACCAG
ATGAAAACCCCGAAGCAGCATCAAAACATGAACAAGCAGCGTTACGAACCAAGTATTGCTGATCGTT
TGGATAAAGCTGGATTGGCTGAACCAGAATATGAACTGAGACTGATGGTGAAGATAAAGTGTCTG
TTATTGATTGGATGATCATTTAGCTGATAGAAGGACTTCTTATTATGATGGATCTGGAAAGAGAG
CATCTAGAGCTTCAACAACATAACGTTACAATGTTCAATTCCAGTTCAGAAAAAGACCAAAATCCA
AAGTTCTGATTTGCCAAAGAATGATTATGATGACACATTTGTGAGTAATAGTGATGAAGTTCATA
AGCGTCAGTATAAATCGATGGTTTCTGATGAGTCTAGTGCATCTGATGATGTATTTGATAAGATTA
AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTGGCTAACGGCAGCTTACAAGTG
GTCATAGAAAACCAAGATAAGACATTCTCAACCGGGCCAGAAATGTTGATTCTTCAATTTGAATG
GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTTCGTGGTAACAATTCAAGTGGTCATGATGATA

GTGTTCCACCACCACCGCCAGCTCACAAGGTGAATAAAAAACCATTGGATGATAAGACGAATTTCC
CTCCACCAGAAGTGGATCCAAAAAGAAAAGGTTTCATTTTTTAGAAAACTTTCTTGGGGATCCAAAA
AAACCATTGAAAAATAACAAACGCCGCCACTAATACCACGACTCAACAACAATTACCAAGTCCCTG
CTGAATCAAAAGAGGAGAAAACCAAAAAGTTTCATTTTTTCAGATGGTTTTTCGTTCATCTAATACTCCAT
CTGCTGCTGAAATTAGAAAATTCAACACCATTTTACCTAAACATGAAATGCTCTACTGCTTTATTG
CTTTATTGAATTTCTTGGTCTAATTTTGGTTTTGAAAGATTTACGGAATGATCAAGTTGGATATTATA
TTACTGGTGTCTATTTCTAAACATAATTTCTTTTAATTTAAAGAGTTGTAAATTTAGAATTAAGATTA
ATCAAAGAGATTTTAATCAAAAATCAGAAATTGTTTGTGTTAGAGTGAAAGGATCTAAAGTTACAA
CTGATACTTTATTTTGTGAAATTGAAAAGGTCTTACTCAAAGAAGGTGGTTTTAGATAAATAA

YDR507C_homolog 1349aa (SEQ ID NO 336)

MPHSRQPSISSIMSQSNHNHPQKIGPWKLGLKTLGRGATGRVLLATHQTTGQKAAVKVVSSELQD
EETEKNGDGLPYGIEREIIIMKLLTHPNVLRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE
VEAIKYFRQIILGTAYCHALGICHRDLKPENLLDSQLNVKLADFGMAALESNGKLLTSCGSPHY
AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLLKVQAGNFEMPVDEVSRARDL
IARMLEVDPMRRISTEKILRHPLLTYPMSNEDLISEKSLPHPTGYKSLGSRVNRIDKQILSNLTI
LWNRDPEEEIVDCLLKDGSNPEKTFYALLMRYKHNDQDNTNNNSPKKSTSFNNKVVRSGSKYSLNG
TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYRSPYK
SPSKRYSYNQSPQSPYGRRSNSQRQFENEPLKAKPRNIYNEIVDAQSNFSLPPSLPPSLPSKDSR
YIMDEPNQPLQPPALSQVPENPIVDSPDLMSAKISSGKRNSIIIGKNNNSNSNKRMSKRKSIR
ASMTTGLKRNSITMKLLSTYAKLSGDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP
EEKEAKEYERLMELERKKHEAELKARRELEKKRRQKRSILSSKKLSIIVKNDADPNNSQELVD
EGIKQPKRQSKNLTAALRALSEGHAASEELTLEDVENLKRRSASQVPVKRRQTPVLTRRPVSRLDPL
WQAHENEQLDRAKDALEQEWDRDSQKRSSSTVSRKKVNRESMSVMDDIVEEDQGRVNRSTRNTYYE
RERDYELPEPTVEDSNLTDYMTETIRKSRLNSQLNVRDPLNEKRKSEPKTLISNVQIPSVTRKSR
NFTTSNKRLSVLSMYSTKESYRDLNSIINSPDENPEQHQNMMNKPALRTSIADRLDKAGLAEPYET
ETDGEDKVSVIDLDDHLADRRTSYDYGSGKRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT
FVSNSDEVHQRQYKSMVSDASSDDVFDKIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG
PEMLIPLHNGGISSQPMKVRGNNSSGHDDSVPPPPPAHKVNKKPLDDKTNFPPEVDPKRKGSF
FRKLSWGSKKTIENNTNAATNTTTTQQQLPSPAESKEEKPKSSFRRWFSSNTPSAAEIRKFNTILP
KHEMSTALFALLNSWSNFGKDLRNDQVGYITGAISKHNSFNLKSKFKRIKINQRDFNQKSEIVC
VRVKGSKVTTDTLFCIEIEKVLLKEGGLDK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118
(SEQ ID NO 337)

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TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA
TGGTATACAACTAAAATGGAATTATTTTCAAATATGCAACTATCATTATGACTACTACGACAACAA
TTTTAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATACCAAGGAAATATCATTAAGA
ATTAATAGCTTTGCAAAAAATTGGTTTTACTCATATTATTTGTTTTAGTTGGAAAGCGATTACATCA
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AATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTTGGGGTTCCGAAGGTGTTTCCAGAAAAA
CCAGAATTGCTGGTGTGCTTTACCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA
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CTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCACGCTGCTGAAGTTGCCGATGCCAAGAGAT
CAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCTGTTGACT
CTCAATTCGGTCTGTTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG
ATGTTACATCTTGGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)

MGISRDSRHKRSATGAKRAQFRKKRKFLGRQPANTKIGPKRIHSVRTRGGNQKFRALRVETGNFS
WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTSAVVQIDATPFRQWYENHYGATLGKKKGGAAHAAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY
LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTGTG
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AATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAAGG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCACAGCAATATAGCAA
TCATAAATAAATTGCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTGAATCTTGTTTTTTT
TCGACATACACCATAAATCCCATAGAAAACGTGCAAAATGTCTGACGCCGGAAGAAAAACATTTCT
ACTAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGCTTACCTTGGAAAAGGGCAAGGAACAA
GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAAATCTTTCACCTCA
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGCGAACAAGACCCTTGCTGAAACAGCTCAAGAATATGTGAGGTTGCCAAAACCTG
AAATTGGAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVSTLTKAVGNSNVPDNQKSFTQTVADSVQQGSDN
AKADLKKQSEQAEGEQRPLSKQLKNMSRLPKSKLERSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTG
TGACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTCTC
CAAATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCACAGCAATATAGC
AATCATAAATAAATTGCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTCTTGAATCTTGTTTTT
TTTCGACAAACACCATAAATCCCATAGAAAACGTGCAAAATGTCTGACGCCGGAAGAAAAACATTT
CTACTAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAAC
AAGTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAAATCTTTCACCTC
AAACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAGCAGAGGGCGAAGCAAAGACCCTTGCTGAAACAGCTCAAGAATATGTGAGGTTGCCAAAA
CTGAAATTGGAAAGGCTGCTGAATACGTGAGTGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVSTLTKAVGNSNVPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTAT
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTCTTCTCGAGTCTTGGTATCGGTTGTAAACG
TATCTGTTTCACTTATCAGTATCGTCATTTATATTAATACTACTTTCTCCTATGGTTATATATTGGT
AAACAAAGAAACAAACAAACAAAAAGAGTAGTAGTTTTGAAAATTGTCAATAAAAGAAACAAAG
AATGAAAGAATGATTGAATGAAAGAAAAAATATGAAAGTGAGTGCGACATAATGTAGAAAAA
TGTCGAATGTCTTGAACCTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAACAAACAGAA
AGAAAGAGAGAAAGAAAAATTCGCCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC
CAATTGATCATTACTTTATTCCACACAATTCATAAACAATGTCCAATTCAGCAGGTTTTGATAGAC
ATATCACTATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT
CAGCAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA

TCCCAGATAAGTTATTAGATCCTAAAACCGTGTCATATATTTTAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAGTTTATCAAGAAGAATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAAGCTTTTATTCAAGTTG
ATTTTGTGATGAAGGTAGAGGTCCACAAATTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAAGTGAATTCAGAAAAATGATATTGAAATTGGTGTGCGCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGYEMPVESLSRRMANISQLYTQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQOEATTYLEKKFKKTDVKGDWQKTV
EFAIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGTCTCAATGTACACACACACGACCAGCAGTAGGAAAAAACA
AATTAAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA
TGTGACATACCATATAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA
AGACCAGAATGTATAATGTTATAAGATAGTGATTTATATTGAAAACACCCTTAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA
ATCATTTACATATAAATAATGAGAGAGAATTACAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGTCCTTGTTTCATTATGTCAAAAAATCTATAGTTACCTACCTCTACATCAATTTATG
GTCTGAAATACTAACATTTTTTTTATTTATAGTGAAAAATGAAGATTGAAGTTGACTCCTTTTCAG
GTTCTAAAATCTACCCAGGTAGAGGTACTTTTATTGTGTCAGAGGTGACTCTAAAATTTTTAGATTCC
AATCCTCAAAATCTGCTTCTTTATTCCAACAAAGAAAGAACCCAAGAAGAATTTCTTGGAAGTTT
TGTACAGAAGACACCACAAAAAGGTATTTCTGAAGAAGCTGCTAAAAAGAGAACCAGAAAGACCG
TCAAGCACCAAGAGCTATTGTCCGGTCTTCTTTGGAATTGATCAAAGAAAGAAGTCAAACAAAC
CATCTGACAGAAAAGCTGCTAGAGACTCTAAATTAGCTAAAGACAAAGAAGCTAAAAAAGCTGCTA
AAGCTGCCAGAAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGCTTCTGTTGTTTCTAAACAAC
AAGCTAAAGGTTCTTTCCAAAAAGTTAAAGCTACCTCCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)

MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE
AAKRRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAARKAEKAKAVA
SGASVVSQQAQKGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT
CCATAATTTATAATGGCATAACCTTTGGATTACCTGTTAATTCATCAAATAATAACTTCACATCT
AATACTGGTCCAACCTGATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCCTGATTCTT
GGTAACAAAAAATCTATAATTTAATAAATTATCGATAGAATCTCTTCCAAAGTACAACCAATTT
CGATACATTTTTTTCTATGAGATGTTTTTTTCCCTTTGTCTTTAACTAATGTATTTGGGTACACT
ACCTGAACCTACCAGTTCAGTTTCAGTCTAAAAAATTTTTTATTATTGTTGTTTTTACTATCCC
TTTGCATATATTAATAATTTATCTTACCCTTTTCATCATGGATACAAAGGAAATAAGATCTACCG
TATCTAATCTTGAAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG
GGGTTAAACCATCCGAAAACTCTTGAGAGAAACCAAAGTAGGTGTAGCTGTCAACAAATTCAGAA
GTCACGACAGTGCCGAAATCAACGGTTTGTGTTAAAAAATGATCAGAAATTGGAGAGATGCCGTGC
AAGCCGAAAAAGAACAAAAAGAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA
GCTCAGCAATTTGCCATCATCATCGGGTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA
CACCATCGGCTGCCCGTAAAGGTTCAAGAAATCCAAAACTGACGGTGTAATATCAATTAATACG
AAAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

CACCAAAACACATTTTGAGAATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA
AAGTAAGTGACAGTTATAGAAATAGGTTAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTCATTAATAATGACCCCTA
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATTGAAAAATTGCACAAACAAAACCTGTTTGATG
CTCAAGGTGCTACTGAAAAGAGAGCAGTDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNRLRSF
AGGTCAGTTATTATCAAAATGCAAACCAGATCAGCGGATGAGCCTTAACTACATTTTGTACTTGTG
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

YGL043W_homolog 305aa (SEQ ID NO 348)

MDTKEIRSTVSNLEKAVDDTTILKLLNILNDGVKPKSEKLLRETKVGVAVNKFRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKLAIAAGTGTTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTS LAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNRLRSF
TMNLRNKKNPRLRERILSKQILPAFIKMTPNEMAPEALKKEIEKLHKQNLFDAGQATEKRAVTDR
FTCGKCKHKVSYQQMQRSADEPLTTFCTCENCGNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon

1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)
ACATTTATTGTTGGCTATACTTTCCAGTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAATGTGTTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCTGAGACAAAGGGTAAG
CATTCGTACCAGGAAGTCTGGAATTAACCGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT
TTGTGTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGACTTTGTTTGAAAAAAT
AATACATGCAAATACTGCATATTAGAATTATAAGGGAATGAAAATGAAAAAAGAATAATTT
TGTAGATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTTC
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCCTT
TTGAGTTTTCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAACTAAAACCAGAA
AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTAAACGGATGAAAGAGTATTGA
ATGTTCAAGGACATATGGAGATTAGAGAAAAACATGGAAAACTAATCGAAAATGAATAATGAATGG
AAAATTTTTTAACTGAATATCAGAATAGACACAACACACAGATCCAGAGTCATTATCACATTGA
TCATACAACCAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTTCAGAA
CAATCAAGTTTATCATTTACAGAAGACAGTTCATCAATATGTCCAAAATACTCTTTGAAGTCAAT
TAAAGTCAAATGAACGAATTACTAATTATTTTTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC
ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTTGGATA
AATACCATCCAGGTTACTTCGGTAAAGTTGGTATGAGATACTTCCACAAACAACAAAACCACTTCT
GGAGACCAGAAATCAACTTGGACAAATTGGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT
TGGGTAAAGGTAGATTACCAGAAGTTCAGTCATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG
AAGAAAAAATCAGAGCTGTTGGTGGTGTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)

MPTRLTKTRKHRGNVSAGKGRIGKHKHPGGRGKAGGQHHHRTNLDKYHPGYFGKVGVMRYFHKQON
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLEVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO 351)

GCTATCAAAATCACTGTTTCAATGGTGACAGAAAAACCGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGTCTACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTAAAAAAGATGGTCAAGATTACGTTGAAATTAGAAATTTT
TTGGGTGAAAAAAGAGTTAGAGAAGTTAAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCCTTGAAGCTGTTTCTCAAAATGCTGCTGATATT
CAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTAAATTCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

AIKITVHNGDRKHVAALRTVKSLIANLITGVTKGYKYMRFVYAHFPINVNIIKKDGQDYVEIRNF
LGEKRVREVKIHEGVTMEISSSTQKDELIVSGNSLEAVSQNAADIQQICRVNRKDIRKFLDGIYVSE
RGTIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAACAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC
AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAATTGTGCAGCATCGAACAATATTGCCAGT
TGCATAGAATAAATCGGTATTATTACGGCATAACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA
TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTGCTGTGTAATTTGGTGAAT
GAATTGATCAGATGATCCTATGGGTGGCATTGTTAAGGTTGTTTCGCTACGATGTAATTTCTAGGATA
ATGAAGGTAAGTACGAACCTATGAGTTTTGATTTCTTCTCGATGTTTTTTTTTCTTGTTTTCTT
TTGTCTGTTGTAGCAAGAAGAAAAAAGTGTCTTCACAAGTCTTGGACTCAATTTTCAACCCCT
CCACAAACTCAATTTCAATTAACCTATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA
GTGCATCTCAGGCTCATAAGCTGGATATTCTTGGTGTAGCTATTACCAATAAGTTCACCTGTATCCG
TGTCTAGTGATGGATATGCGAAATTTTGGGACAACAAGCAAGACGAAGTTCATCTGCCTAAAGAAT
TTGTCCAACCTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTGC
CAAGCTCTACATTGAAAGTGACATTATTAGCAATTGCTATGTTTCAATGGATCTATCATCTTCAGAT
ATTATATCAATGATGACTTTTCAACTATCGAAAGTCTAAGTATGATATAAAATCAATTTGAAAGCA
ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA
CCAATGGCACTACAGAGGTTCAATTTATTGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT
TTGAAAAGTTTGGGCAATTAAGGAACTCTTCTTCTTCCCAAATCTTTGGCTATATGTCCAA
CAGAGAATAAAAAATGTGCTGTGGGGTACATCAATGGTGATGTCTTGTATATGACTTTGTAGCT
TGAAATTGATATACACATTTCTGTTTCGAGTGATTTGGTGACCAGTAGAAATTTCCCAATCGACGTCTA
TACCTAGGGTGTGTCATTTTCCCTGGTGGAACTTGTGGCTGTGGCAAGAGACAATCAAGCTG
CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAAATGTGGGGTCTTTGGCCACACCCCTCAC
ACTCGGCCAAATCTGTTGTTGGTGGGTTTGACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG
AGGAAGGTAAGCACTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA
GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG
ACGAGAGTGTGCTTCTGGTGTGCTTTTATTAAAAAGGGGGTTAGAGGTGGCTCTGGTGGTGACA
GCAATGAAGGATTATGTGTCGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA
TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFTVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
AVAAYENVLPSSTLKVTLAFAFCFNGSIIFRYYINDDFSTIESLTDDIKSFESNCWTPGFYRDPES
KQDYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSFPNSLAICPTENKKCAVGYING
DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLAFFSPGGTLLAVARDNQAAGSITLYDVEHGE
NVGSLATPSSHSAKSVVGGFAHQGWILGLSFDEEGKHLASCGFDKICRVWNLETSEREATISISISD
LDDTTHNDQDESVASGVAFIKKGVRRGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATCTGGTGGTTCAGTTAATTTATATCATGTCACTGAACAAGGTTGGACTTATC
ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTTGTAAATG
TAGATGGATAAAGTAAGTTGATTGTATAAAAAAGAATGGATTCATTAATATAAATTTACAAATCT
GATAATAAAGTACAGTAACCTATTATGCAACAATTGAAAGTATCCTGTGTCAAGTATTAGGGCTCA
AAAGCCCTAACAGGTTGCACGTGATGTTGATTTATTTATCCCTGCACACATTGAGTTTTTTTCTA
TGGTGAATAATTATTAGTGAGACGATGTTGTTTCGCATTTTACCACACACTCTCACACTGAGTGTAGT
CATACTAACAATCTTCTCACACTATACACAAAAAAATCTTTCGTTTGAAAAGTTTGAAGGTTTC
GTTTTCTCAATAGTATATCCATACAATAACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC
GAAATGTTTTGTTTTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG
AATTAATTGAAAGAGTTTTCTTTTGGGGAAATGGGTTCAATAAGATTTTCAAGATTGGAATCAAA
TTATGTGCAGATGTGAAGAAGATAAATAACAAGTTCAAATCAATTAATAAATTTTATGTAAAT
ACAACGATTATCAATTACAGTCAACGAATAGAATAAAACAAAAGCCAGCATATAACAGATACCAAGT
GATTCATCCAGTGATATAAATAATGATATTCAATTAATAAACAATATTAAGACATTTTTTATTTAT

GTATCAACAAAATACTAACTTATCTTTCTTTTAAATTAGTCTGACAAATCCCAAAATGTTATGCGTG
AATTACGTATTGAAAAATTAGTTTTTAAACATTGTGTGGTGAATCCGGTGATAGATTAAACCAGAG
CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCAGTTCAATCTAAAGCTAGATACACTGTCA
GAACTTTCGGTATTAGAAGAAATGAAAAAATTGCCGTCCACGTTACTGTCAGAGGTCCAAAAGCTG
AAGAAATCTTGAAAGAGGTTTGAAGTTAAAGAATATCAATTAAGATCTAAAACTTCTCTGCTA
CCGGTAACTTTGGTTTCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG
GTATTACGGTATGGATTTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCACCAGAAGAAAGA
GAGCTAGATCCACTATTGGTAACTCTCACAAACCAACAAAGAAGATACCATCCAATGGTTCAAGA
CCAGATACGATGCTGAAGTTTTGGATAAATAA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)

MSDKSQNVRELRIEKLVLNICVGESGDLRLTRAQVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKAEIILERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGIKYDPSIGIYGMDFYVVMG
RAGARVTRRRKRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTTGTGTGTATATGCGAGAAATG
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATAAAATGTCATATTGACAT
GATAAGGATTTATCAATACTGTTAGGTCTATAGCCCTAACTTTAATCATTTACACGTGATACAAAA
AAGTTGTTTGATCCCGCACGACTATGAGTACGCACTCACTAATTATAGCCTGAAAAAATAATTTTC
CACATAGTAAGGGGATTTTGTATGGTGGTGCCTCGCCTAAGACGTCTGCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCACCAAATAACTTTGCGGACACTCT
CATATACTCAATTTTTTTCTTACAAAAATTTTTTTCTTCTACTTTTTTCAAGAATTCTTCTTTTA
CAATTCACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAACCTGCTAGAAAAATTAAG
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT
CAAATCTTCTCCATTTGGTGGTTCATCTCACGCCAAAGGTATCGTTTTGGAAAAAATTGGTATTGA
ATCTAAACAACCAAACCTCTGCTATCAGAAAAATGTGTCAGAGTCCAATTAATCAAAAACGGTAAGAA
AGTCACTGCTTTTCGTTCCAAACGATGGTGTGTTGAACTTTGTTGACGAAAATGACGAAGTCTTGTT
GGCTGGTTTCGGTAGAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGTAGATTCAAGGTTGTAA
AGTTTCCGGTGTCTCTTTATTAGCTTTATGGAAAGAAAAGAAAAGAAAAGCCAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)

MGKGKPRGLNSARKLRVHRRNRWADQAYKARLLGTAFKSSPFGGSSHAKGIVLEKIGIESKQPN
AIRKCVRVQLIKNGKKVTAFPNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVVKVSQVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTTGATCTCTAAGAAGATGAACAGGCCTTGAATGGGAGGGGTTGGTTCGACTTCCACGAA
ATGTGGTTGGAAAACTTGAGTCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAGAAAAAACC
ACCAAACCCCAACCAACCTAACCTTTTCTTCCATCCATTCTCTTCTTACTTTGCAAAATG
TTGAATCCAGTTATATTTCATTAAAGATCCTATAAAATACGATTATTCACAATTTATTATATCTTTA
CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAAT
CAATTGAATGAAATTTTATGTTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT
GATGGAGATACCGACAGTTTGCCTATGTTGATTATCGATTGAAATTAATATATTTAATTATTA
TCAACAAAAAATTGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT
AATGATAACAGTACTAATTGTCATCTTTGCCATTGTCAATAACACAAATATCAAACATTGAAATT
CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAATTACTACT
AGTCGGCAATATCAACAATTTAAAACCTACTGCTGTAGGTGGAACATTTGATCATTTACATGATGGT
CATAAAATTTTATTATCAATGGCAATTTTTTTAACTTCAAATAAATTAATTATTGGTATAACTGGT
TCTAATTTATTAAATTAATAAAAAATTTAAATCTCAATTACAACTTTTAATCAAAGACAAAATTTA
TTAATTCAATTCATAAATTTATTATTGAGTGAACACAGTGTTATTTTTTTTGAATTTATGAA
ATTAATGATGTTTGGTCCAACCTGGTTATATTAATGATAATTGATAAATTAATATCTCAAGAA
ACTAAATCTGGTGGTGAATTTGTTAACAAATTTTCGTAAAGATCATGGATTTAAATATTAGATATT
ACAATAATTAAGTGATTGGTGGGAATATTGAAGAAAATTCATGAAAGGTAAATTAAGTTCAA

CTGATATTAGAGAACAAAGAATATAATCGATTATTAAATCAATAA

YGR277C_homolog 322aa (SEQ ID NO 360)

MLNPVIFIKDPIKYDYSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD
TDGDTDSLPMFDYRFEINILFNLSTKKLNQLCLNNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE
IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT
GSNLLINKKFKSQLQTFNQRQNLVIQFINLLLLSETSVIFFEIEINDVCGPTGYINDIDNLIISQ
ETKSGGEFVNKFRKDHGFKLLDITIIKVIGGNIEENSWKGLSSTDIREQEYNRLLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT
TGGTGGCAGTAGTATTGGTATTAAGTGGGTGGGTGCTGTTATTAGAGAGTGGGTGTTATAAAGAA
GGTTGTGATTTTTTTTTTCCACTGGTGGTGGTGGTGTGCTGATTGTACTGCTGTTCACTTTATTGTTT
CGTTTCGTTTTTCTTTGTTTGTGTTGACGTTGACATTTTTTTTGCTGTTGTTGTTGTATGGGAATT
TTTGTATTAGTTGTTCTTTTTTGTGTTTTTTTACTTGTTCAAAGTTTCATATAATAATAATATTCT
TGTTTTTCATATTTTTTTTTTTCAGAACAAAGAACAAATACAACCTATATAATTTGATCTTACTCTTAT
CCCCAGGTTTTTCTATTTGTTTGTGTTTGGGTTTGCATTTCATATATATATCTATTATTCAAATCAAT
TTGAGGAGTATCATTAATTTAAATTATATCAGTTAAACAATGTCGTATCGTGGTCTAATCAATTTG
GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA
GCAAAAGTCCTTTAGAACAATTTGAAGATGTTGCTAAAAAGTTGAAGATTGGATCGATGATTATT
TTAAAGTCTTGAAACCATACGTCCCAGCAATTGGTAGAGCATTTTTGGTGGCCACTTTCTATGAGG
ATACTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACATATAGACACTATT
GGCGTTGGTTGACCGTTTTATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG
TAATTGCCAGAAAAAAGAATAACATTGCTACTATTGCATTGATCGTTGTTGTTATTATACAAGGTA
TTGGGTATGGTTTTATTGTTTGTGCTCAATTTGTTTTGAGAAACTTGTCGGTTGTTGGAGGGTTAG
TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT
TGAACAATCAAGACAACAAAAAGTATTTCTTTTAGCTGGTAGAATTTTGTAGTATTATTATTTT
TGGGATTTCGTCTTTCTTCTGATTGGTCAATGGGTAGAGTTTTTCATTATTATAATCGGGTTAACTT
CTTGTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTTCAGCTGCTATCATGCTTATTGTTTTAT
TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT
TGAGATATGAATTTCTTCAAGTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG
CTGGTGAATTCTCCATCGATGAAAAGAAAAAGATTTATTAA

YGR284C_homolog 308aa (SEQ ID NO 362)

MSYRGPNQFGNQPPHHGIPSQPQPHIGPISSSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYYLHNYRHYWRWLTVLFLINNMVMTVASTLVIARKKNNIATIA
LIVVVIQIGIGYGLLFDAQFVLRNLSVVGGLVLAFLSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGFVFSSDWSLGRVFIIGLTSCASIVVGKTKFSAAIMLIVLFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLVVNAGAGEFSIDEXKKIY

YGR285C_homolog 1876bp PathoSeq: 1..1215, public: 1216..1876; CDS: 501..1781 (SEQ ID NO 363)

AATTATTAGTTGAAAAACAAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTGTGGAGG
AAGATAACAATGGGAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGTCTTGG
TCACATTAATTGAAAATACAGATGGAAGCAACAAAGTCGCTAAAGGAGAAGGGTCTATAGAAGTAT
TAGATATGTCTGCCATAAAAGAATAAACTAACTAGACAAGTGTATAGAATCTTTTTTTATTAAATA
GATGCTTATCTTAGTTATGTTCCAGAACAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT
TTTTGCACAAACAAAAACGAGAAGATGAAGAAGCAAAAAAGAAAATTTTTTTTTCTCAACCATCT
TAAATCCTCCTACAATTAATTTTCATACCAATAAAGAACATGCTATTGTATTACCATCAGGAACCTA
CTGACGGATTTAAAGCCGCTCCTCAAAATACTCTGCCCCAGTGCCTCGTCCAATTGAACCAGTTGGTC
GTTACTTCTTAGCCACGCTCAAGAAGTTGCGTGGACACACTTGGTCTGAATTTGAAAAATTGG
AAGCTGAAAAGAATGTTAAACAATCGAAGTCAACGAAGATGAGGATTGGGAGATGAAGAACAAA
GTGAAGAGTTATTAGAACACGATCCAAGAGAATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT
TATCTCATTTGAGAAGTAAAGCCACTGAAGATCAAATCAGAAGAGCCACAGAAAACAAGTTTGA

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAAAGATGGATTTTTCAAAATTATTC
AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA
ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG
AAAGTGAAGCAAGATTTTCTACTAAACAACCAGTTCATTGTTGGGAAATTTAGAAAGCACCAAAG
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGGAAGACTTTTGAATTCAAAG
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAACGTTATATTGAACGTAAGAATATTG
CCCAACAGAAAGAAATTGAAGCAAGAAGATCACAAGAGATTATCGAATTGGTTCGAAAGAGCTCATG
CTGAAGATCCAAGAATTAATTTGTTCAAAGAAAAAGCCAAGAAAGAAAAGGCTGCTAAGAAATGGG
AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAGGCTGCTGAAGAGGCCG
CTGCTAAGAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACTCTAAAAAGCTAAAGAAGCTG
CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG
GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG
TCAAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAATCTACTTTTG
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTTGAAATATTTTAACT
AGATTTTTTTTTGTAGGAAAATAATATATATAGAATGTAACTATCAAAAACAATTATACAGAAG
CTGAACCTCAAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKA VSKYSAPVRRPIEPVGRYFLAHASRTLGRHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHDPREWKTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHPDKKSASGGL
ENDGFFKIIQKA FEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFEAWGPVFESEARFSTKQVPV
LLGNLESTKEEVD AFYSFWGRFDSWKT FEFKDEDVDDTANRDHKRYIERKNIAQQKEIEARRSQE
IIELVERAHAEDPRIKLFKEKAKKEKA AKKWEKESGSRKAAEEAAKKAEEAAKKAEEAAALK
ANSKKAKEAAKAAKKKNKRNI RAAVKDNNYFGDSAKSADIDADVDLLIEKFDDVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLK YFN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:
538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAATAAGTC
ACATCTCAAATTGGTAGTAGAAGAATTCAACCTTGGGACAGTATTCTCTGCTTAAATGAGTTTAC
TGATCAAAATAAAATATTGGCTCAACCATTGAAAAGCTATTCTTGACACTTTTTGCAGTTTGTAGTTT
TGGTTGTTTCACAATTGAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT
ATTGCTTTGAGTGAAAAGTGTACATTTGTACACACACAAACAAAAAATACTTCTTCCCCCA
ATATGCTGCGTATAGTGAGAAATCTTCTTCTCTTGGCATACTATCGCATTTTTTTTTTGGTAA
CTCACGAAACCTAATTGGAAGAAGAAAAAGAGAAAAAATAATTTTCAGTTTTCATAGATTTT
AGTTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTCATTAGATTTACCATGAG
TTATGGAGGGATATTCTTGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC
AAGATATAATTGAATTGAAATAAAAAATTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC
AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT
TAAAAGAACAGGAAATGAGAAGAGAAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA
TATACTTTTGGTGTGGATCCATGTGTTATTACTGAAATCATCGAAACGAATATAACCCTCCTTTTC
CCACATTGACATAACTCAGACACAATCTTTCAAATAAAACATGTAATACTAATACTATTATTTTTTTT
TCGTATAGGTTTTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT
TGAAAACCTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA
TCACCACTGTTTTTCAGTCACGCTCAAACCTGCTGTCACTTGTGACTCTTGTCTACTGTTTTGTGTA
CCCCAACTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTCATTGAGAAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHPSPEAKQHKLKTLVQQPRSFMDVKCQGCLNITTVF SHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1:
501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
TTTATATTGTTTTTTGTTTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTTCATGTAATT
GTGATGTATTTTTTTGTTGGTCCCTTCTTTGTGTTTTGATATTTTGCAGCTGGTCCGATCATACAA
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAACAGGAGACTTTTGGAATTTCTTG
GTTTAGGGCTCTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTAAATTTGTGCGGTGAAAA
ACAGAAGCGAAAAAAAGAGCTGGAAGTGTGATTAACAACAACGAGGGAAGAAAAAACTTAA
TTAGGTGAACAAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTCTCACGCA
CTAACAACTCAACCTCCATTGTGAGAAAAAGAGATTTTCTTTGAAAAAAATTTACATACATATC
TTAGTTCACTAGTAACCTTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC
AACAATGAGATACAAGATATTCCTCCAATACAAAGAGATTAATGGTGTTTTTGATAGAGTGTAAG
CCATGTGTTTTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGAAATTTGCCAAACAACAT
TGAAACGAATTTTCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAAATTAAG
AAAACAAGTCAATATTATCAAAGATGGAGTTTTATAAGGAGAGATATTGAAACATCAAATTGTTGA
AAGAAATAGCCAACTATTGTCACCATTTCCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT
ATAGTTAACGTTCCAAAACTAGAAAGACCTACTGTAAAGGTAAAGATGCCGTAAACATACCCAA
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTTCGCTCAAGGTAAAGAAGATATGAC
AGAAACAATCCGGTTATGGTGGTCAAACCAACAAATTTTCCACAAGAAAGCCAAGACTACCAAA
AAAGTTGTTTTGAGATTGGAATGTGTTGTCTGTAAAACCAAGGCTCAATTACCATTTGAAAAGATGT
AAACATTTGCAATTGGGTGGTGACAAAAACAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK
KVVLRLCEVVKTKAQLPLKRCKHFELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID
NO 369)
GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT
TTCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGTTTGAAGTTTGAATTTTCAAGAGGAGA
TGACGGTGCAAAAAGATCTACCACCAAAGAAGCACATAATTTTTTGAATGATTCACGAAAGAGTTT
CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTTCACGGGAAAGCAG
CAGCGGAAGTTCAATAATAAAAATTGATCATCTAATGTGGACGTGTCAACGAAACCGGAAAA
TATAAATAGCAGAGATAACAAAACCTGAGAAGAATATGACTTTGAGTTCAAGTCAACCAAAACCGAG
TGTCGAAGAAGTTAGTAAATCTTTGAAACCAACAATTACCAAGAAAACCTTCACTGATTACTTT
AAAATCTGCCAAAACCTAAGGCTAAAGAAGAAAAGGTAACAATCGAAAAAGTGACAAAACGATTAA
TTCAGAAGAACGAAAAACGGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAGGATAA
TAACTGGAACCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG
CTGTGCCCTAGGACCTGATAAGAATACTGGAACCAACGATTCAGATAAATCAGAAACGACTCAACC
AAAACCTTGCCCGCTCAGAATCATTGCGGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC
TGATTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTTCAAGTGTGGCAGCAA
TGTGCTGGAGAACATTGATGAGAATGAAAATATTTTCAAGAGCTGAAACTGTTATAGCAGATGACCT
TCCACGTCTCGATGAAGGAAAGAACTTTTACGTGAACAAAACAGCAGATGTAAAGAGACATAAATT
GAAGAAAACAAAATTGAATACTATTTTGTAGTTCCGATGAAGAGGAGGAGAGATTCAAGAACCAGA
TTTCAAACCTCAAGAACCAGAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAATTTCAA
AGCAACAACAGAAATCAGTAACGATAAAAACAGAAGTAAATAAGCCAGAAAGTGAAAGAGGTTGGCGA
GAAAGAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAGAGAGAAATGCGGTGCGAGAA
TGCAAAGACATCTGAAAACGGTGTGCTAGTTCAAATCAGAATCTAAGATTTCAAAGTCGAAGAACT
ACCTTACAAAGTTAAACGTGATTCAAGTGGTGCATCATTATTACAACGAGCTTGCAAGAGGTTAA
TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAATGAAAAGGATTTCTGTGGATT
CACATGCTTGCATGAGGCAGCATTGGAAGGTCATACACAAATTTGTGAAATATCTCATCGAAAATGG
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGAATTCGAGACACCATTGATCGATGCAGCTGA
AAACAAACATCTTGATTGTGTTAAAGTGTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT
TGATGGATTACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT
TATTCAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTTCAAGTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACCTATTTTGCAGAGCT
AATTAAAGGTAAGGGAATATATAAATACGCTGCAGAGAAATCAAAAAGAGAAAACAGCAGAATATTT
TGTTGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAAACGGCCACAC
AGAAGCTGTTGATATTATAGGGCTAAACCCCTACACCTTTTAATATTGATACCGAGTCAAGTTG
TGGTGTACTGCATTATTGGCCAGTATTGGACGCGGTCATTTTGAAGTTGTCGATTCTTTGTTGTC
CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTGAATGCTTTAGAAATTGCACAACA
CTCGCCACATTTTGATTACGGGAAGTTAGTGTAATAATGAAATTCATGGAGAAGAAGAGTGGAAC
CAAATTTTGTCTGGTATTCGGTCAAGGGTAGTATCTCGTGCAACATCTCGTGACCTTCTGTTCC
CGTATCATCAGACGAAGATGACGTAGTGGAAGAAAAAGAAATTACAGCACACACAGAAAAATAAAG
TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTTCAGCAATCGGAAACC
CCACGAGTCTACAGGTCGAAAACCTGAAAAGACTTAGCAATGAGGAAAGAAAGCGGAAACGTGA
ATGGTCAGACGATGAACCTAAAGAACCACATCTTTGAAGAAGTCAAAGTCTGATTGAAATTGAA
ATCACTACATAGAGAATTCACCTCTGATGATCACCACACCAGTGAAAGCCATTTCAGATTCTTTTGC
AGAAAAAAGAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCTTC
TCAAGCAGTTATCAAGGCACAAGAAGAACAAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA
AGAAAAGGTGCAAGCTAAAAAGAGGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAGA
GCAGAAACGGAAAGAAGAAGAATTTGCGAGCACAGAAGAAAAACGAATTGCCAAAGCAAAACA
GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAAGTGAAGAAAAGAAAGT
GGGGTTGCGACAACAGTTGACATTAGATCATTTACCGGTTGGATTGCGTTATTGCAAGTTTGTATG
AAACCCAAATATCTCGGCTGTTGATAAATTTTGCCTTTCTATGTATTGTAATCGACGATAAAAA
GTATGCTGTTGATTTGCAAGTCTCCTTGATCAGTCAACGGTTGTCAGCAAGGTTATCAATACTGT
ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAGCAAATTTGTGGAAGCTCTTTTTCAA
GTTTATTGGTATTGATCCTAGGAATCCAAATTGTGATCAAAGAAGCTCAATAACAAATGGTCAAAA
ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT
TCCAGAAGTCACTCAAAGCAAAAGATAACCAAATTGATGTTAGTTTAGAGTCTTTGAGTGGGTT
TTCTGATTGCGTCAAGGATGATATAATGATGTTGGAATCTTGAATTTGATATTGATTCCAAGAA
AATCGAAAAGTTTATTCCTCCTCATTTGAATACTAGGAAAGACATTATTAGGACTGTCAGTACTTT
AGCACACCCACTATGGTGA

YIL112W_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKTSFTDYLSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ
SEQLLTDKKDNKSEPNSEVNLKDNNDSDKATNGCALGPDKNKTGKNDSDKSETTQPKLARSEFADT
SLLSPVNESDITDFNLAELIPEAKDGSVVAANSENIDENENISEAETVIADDLPRLDEGKLLR
EQTADVVRHKLKTKLNTIFSSDEEEEEIQEPDFKLQEPEKLPEDDQHPDFQNSKATTEISNDKTE
VNKPEVKEVGEKERNHQLDRLPIKKEKMRSENAKTSSENGVSSKSESKISKSKKLPYKVKRDSSGR
SLLQRAKCKGNFADVDYIERGASANEDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG
DSETPLIDAAENKHLDCVKVLLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEEATANY
NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIYKYAAENSKEKTAEYFVAGHNLEGKPD
ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRHFVVDLSLLSKGADPFKTRKK
DGLNALEIAQHSPHDSREVSVMKFMKKSGTKILSGIPSRVSRATSRAPSVPVSSDEDDVVEE
KEITAHTENKSAEKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDPEKPHL
LKKSksDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPPPSQAVIKAQEEQK
IKDAEEARLWQEKVEAKKRARREMLKSEKEKEQKRKEEEELRAQEEKRIAKAKQEEQERLAREAE
EKSKELEEKKVGLRQQLTLDHYPVGLRYCKFDGNPNISAVDKFLPFYVFVIDDKKYAVDLQVSLIT
STVVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCQDRSSITNGQKQFQNLHLHFE
VDLAEFLKEFPVHSEKAKDNQIDVSLSELSGFSDCVKDDIIVDGNLEIDIDSKKIEKFIPPHLNT
RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGATTTGCCCCACTAAAAAGAAAACCAAT
GAAACAATAAGATTGATTGATAGATTTGGTTGTAATTAATCTGATGCTTTCAACATTTGTTTTTGT
TCGTGTCTCGGTCATTGAGGTGGGTAAATTTGTTTTCTTTTGAGAATTGTGAGCATGCAATGTCG
CATGCAAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCACGTGCGT

127/161

TAGTTTTAAACCTAAAAACAATTTTGTGCAGTCGTGCACCATTTCGTTCTATTTTTCTACTGTGA
TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTGCGATTCTCAAACCTCTCTCACAGGCTTG
GTAGGAATGAAAAAATTTTGGTAAAGGCGAAAAAATAAACTTGAATATTTTGGGAATC
CCCTTTTGTATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCCTTGAAAGCTTTAG
CTTCAAAATACAACGTGTGAAAAATCCATTTGTGCTGTAATGTTACGCTAGATTGCCACCAAGAGCCA
CCAACGTGCTGTAAGAGAAAGTGTGGTCACACCAATCAATTGAGACCAAAGAAGAAATTGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)

MIEPSLKALASKYNCEKSICRKCYARLPPRATNCRKRKCGHTNQLRPKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
501..2294 (SEQ ID NO 373)

ACTCAGCCTTTTGAAATTCACCTTTTGGTAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT
CTAACTCCATATTTGTTGTTCTTACCCTCTTGCATAGAGACTTTGATCGTGACATTTTGTAAAGTGG
TAGAGGTATGGGTAAGATTATTTTACCACCGTTTCTTTAGCAAATAGTCTAAAGCATTCTCTG
AATTGTTGAGTTTCGGTACATCATTAGCTATCTTTTGTACAATTGATTGCTTCTACCTCTAGTCA
TGGAAATAACAAGTTAACAGCGTGTTTTGTGGTTTGTGGAACAAATAAATTTGTGGTGTGTAAT
GTGTGTGTTTGTTTTTTTTTTTTACCAGCATTTTGTCTTGTCTTAAAAATGAAACAGCGCAATGAT
TCTTTTCATAGTTTTTTTTTTTCCATACATAACTTCTGACGCGTGCACTATATCTGCTAACATACTC
GGCAACAACAAAGAAAGAGAATTTGAACATAATCCGAAGATGAACGACCCAGAGATGAACAAATTG
ACTCCGATGATGTATTAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT
TGAAATATGCAGAATTAAAGAAGAACAAAGCCTTGAAAAACGTCGTTACAGTCACCACTGGAAG
ACATGCTGAATAAACAGAAACCCCATCAACCGGAGGTCCCAGAACCCAGAAAAAGCTAAAGTCC
ATTTGGATAAGGTAGTAGAAGAACCAAAGCAAAGAAATTTTACCAAGAAGGAGCCTCGGGATTCCA
AGATAAAAGAATCAAACCTCTTAAACAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG
CCCATAAATAGATTTTCAAGTAAAGAGGTTTGAAGTTTCAATTGGATAAGTATACTTTTACGCCAA
AAGACGTTGTTGATGATTTAGAACCGATATCCAAGCTTTTACTTGCGCAGAAGATACCTTGCCCAAC
TGCAAAATGCCGACATTATTGCGGAACTGATAGCAACATGAAATTCTTAAAAATTGACAAGTTTT
TAGCGAAAACCCATAAATCAAACAACTATGCTGAACCCAAGTATTGTAATTGGTGTCTTGTGCTT
TTGTGGTGCGCAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG
GAAATTTTATGAATTCTGTAGACTTGATGCTTTTGTATAAGGCTTTTCAGAAAAACGGGAAAAATCC
AACCGGGTGATTTATTATTCAATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG
GCCAGTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAAACCAATGTGTCAAGTATTTTAGAGATAG
GATCGTTAAGAGATTTTGGGTTTGTGCAAGTTTACTAGAAAGCTAGATAATAGCAGATGCAAAAGGG
CCATCAACACAAGGACGCAAGAATTCTGCGATATACATTTGGATATGAAGTTTAAAGTCTAGTACAA
GAATGGAATTAAATGGAAGTGTTCGATTAGATCCCCGCAAAAAACAAGAAAAAGATGTACATGA
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GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAAATCAAGCGGCGCA
AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTCCGGCTTCAT
TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCGAGTGATCGTCTGAAGA
GCAAAGGATTCACCAACACAATGATTTACATATTTGGGTTTGATCCAACAGGTACATCTTTGAACC
AAAATAGTACCCTGCTTGGCAGCAAGCTGATGGAAAAATCTCGAGCACGGAATTGCATGATTTGA
GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA
AATGGAACACGAATATCAGAACTTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA
CCTCTCGTCGGTTACAGAATCTTGTAGGAAAGCAAACACACGCTACACTAGTAGATAAAAGGAAAA
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT
TTGACGACGAAAAGTCTAAGATGTCTACATGAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)

MNDPRDEQIDSDDLTSSDELKDLVQEFELKYAELKKNKALKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVEEPKQRIFTKKEPRDSKIKESNFLNKLYETSNKHDKEDAHKIDFSKRREFE
QLDKYFTFPKDVVDDLEPISKLYLRRRYLAQSQIADIIAETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANNSKYIKLVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFCFKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPQKNKKKMYMNKNGSGFIKQYNEESTVIGTSYGSPLPDKRYQDPK
VLQNIKRRKLIDDKAKEMLEQKLSKLGSASLLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG
FDPTGTSLNQNSTSLGSKSMEKSRARELHDLVETSGHKSLSSSSKQDRQSKVAKWNTNIRTLQNYD
RRVASHSLSTRRLQNLVGKQTHATLVDKRKRVVVSDDEQPGMEEDEEDIEIQFDEKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG
GCATCAAGGTAAAGGAGGGAGTTTGGTATAGTTAGGTTTTGACTTATTTCCTTTTTGGAGTAGA
TATAACAGAACTACCAAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAAATTGAGAAAACCAT
TTATGCAAGTCGTGTACTGGTGATATTCTTGGTCAATTGCTACACTTTTGTAATGAATACTGTAAT
GTAGCCGACGTGGGTGAANAATATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA
AATATAACAAAATGTTTCAATGTAAACTGATGGTTAAGGGATTATAAATCAAACGAGTAGTGCTT
TTGTTCCATAAAAACCCATCGTGGTGGTAACGTCAGGAGACCGCGACATCAAATGGAATTCACACA
ATCAGTCTCCGAATTTATTACCCCTGAAACTTAACCTTAATGAAAGAGCCTTCCATCACTACTACCT
TTGTTGAGGTTACAGACAAACTTCCTACAAAGCCTCCGTGCAGGGTGTTTTTCAAGAATGAGTATG
AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCATGGGACACTTGGTTGGCCAGTCTATAGATTGGG
CCAGAAAACCTTGGCAAAATCGAACGTAGCAGTTTTTTCGTCATCTGGTGGTAATGCAGGATTAGCAG
CTGCTTATGCCAGCCAGTTTTTTTGGAGTATCGTGCACGTGTTGCTGAAAGTTTCAAGCCAA
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG
CCGATAACTATTTAACTGATTTTGTATTATAAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC
ACCTTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAAATCATCGATCAAA
AGCAATTACCCAACCTTTGATAAAGTTAAGGGGGTCATTTGTTCCGGTAGGAGGGGGTGGCTTATACA
ACGGAATAGTTGAAGGTTTGGAAAATCATAAGGAGATACCAGTGTGGCAATTGAAACTAAACAAG
CGGCCACGTTTGACGAGCGGTCAAAGAAGTTAAAGTTGTTTCATTTACAAAAGTGCAAACTTTGG
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACATATATGAGCGCTCTACAG
TTCTTGCTGAAATTGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTCCGGAT
ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA
AATTTGGTACATTAAGTCCAGATGATATTATCATTGTTGTCATATGTGGTGGATCGGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)
MKEPSITTTTVEVTDKLPKPPCRVFFKNEYEQPSGSVKLRGMGHLVGQSIDVARKLGKSNVAVFS
SSGNAGLAAAYASQFFGVSVTVVLPESKPTVIEKLKSLGADVIIHGKHWEADNYLTDVFIKNL
DKTVYPVYCHPDDPLLWEGHSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVVHLQKVQTLATSLAPYLSSKALANYIERPTVLAIEDDLDAVKG
VVDVYDHFVGYMVEPACGASVASVMHRQDLLNKFGLTSPDDIIIVVICGGSAINKYIIDEYRSLLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:
807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)
TTTTTGAAAACAGAGAATGAATGAACAATTGATGACCATAGAAATGAAGTGAGAACACATAAATCT
GCGACACTTCACGTGATAACAACAAAGTGACATGAACAACAAATGTCGTTTGTATAATTTGCGACA
TTTGTGTTCAAGCCAAAAAAGAAAGACAGAAACAGAAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAAATTAATCTTTTATGGTTGTAACATTTCTAGTATATTCTACGTAATAGGTGAGGTCCCT
ATATGCAGTACACACAGGTTTTTTTTCACAGATGTTGACACAGTGTGAAAATTATTCACGTTGATT
TATAAATATACAACCTTACCTTCCACGGTTTTTTTTTTGATTTTTGATTTTTTGAATTTCTCTTTCT
TTTTTTTGTCAATTTATTTATTAACAACTTCTCTTGAATACTTTATTTGATAAATTTTACAAGATT
TAATTAGATCAATTAGATTATAGAATCATTTCAATATAATGAGATCATCACAATCTTCTTGGTTAC
CACGTATTGGTTTATTATATGTGGCGTTAGTTATACCTTATACCATTTTTGGTTTCACCGAAGCAGC
CATTTGCGGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTATGGTACAGTCATTGGTA
TAGATTTGGGTACCACTTATTCCTGTGTTGGTGTATGAAAAACGGTAAGGTTGAAATTTTGGCCA
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

129/161

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTTCGATATTAAAAGATTGATTG
GTTTGAATATAATGATGACACTGTGCAAAAGGAACTTAAACATTTGCCTTACAAAATTGAAAATA
AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCCTGAAGAAA
TTTCATCTATGGTTTTTGGGTAAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAAGTTACTC
ATGCCGTTGTCACTGTTCCAGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA
CTATTGCTGGTTTTGAACGTTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT
TAGACAAAGGCGACCAAGAAAAACAATTATTGTTTACGATTTGGGTGGTGGTACTTTTTGATGTTTT
CTTTATTGTCCATTGAAGGTGGTGTTCGAAGTCTTGGCTACTGCTGGTGATACTCACTTGGGTG
GTGAAGATTTTGATTTCAAGATTGTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG
ATATCACTGCCAATTCTAAAGCCATTTCCAAATTGAAGAGAGAAGCCGAAAAGGCCAAGAGAACCTT
TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA
CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTTCAGAAAGACTTTGAAACCAGTTG
AACAAGTGTGAAGGATGGTGGTGTCAAGAAATCCGATATTGATGATATTGTTTGGTTGGTGGT
CCACCAGAATTCCAAAAGTTCAAGAATTATTGGAAGGATTCCTTGATGGTAAAAAGGCTTCTAAAG
GTATTAACCCAGATGAAGCTGTTGCTTATGGTGGCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG
AAGGTGTTGATGACATTGTTTTGTTGGATGTTAACCCATTGACTTTAGGTATTGAACTTCTGGTG
GGGTATGACCACCTTTGATCAAGAGAAACACTGCCATCCCAACCAAGAAATCTCAAATCTTCTCAA
CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAAGAACCATGGCTAAAG
ACAACAACAGATTGGGCAAATTGCAATTGACTGGTATTTCCACCAGCTCCAAGAGGTGTCCACAAA
TTGAAGTCACTTTCTCATTTGGATGCCAATGGTATCTTGAAAGTTGAAGCTGCTGATAAGGGAACCTG
GTAAATCTGAATCCATTACTATCACCAACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA
TGGTTGAAGAAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAAGAAAAGATTGAAGCTAGAA
ACTCATTAGAAAACCTATGCTCATGTCTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTAG
GTTCTAAATTGGATGACGATGACAAGGAAACTTTGGATGACGCTATCAAGGAAACTTTAGAAATTTA
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTTGAAGAACAAAAACAAAAATTAATTGACG
TTGCTAACCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG
ATGCCAAATTCCGTGATGATGATTGATGATGAATTCGATCACGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFAVAASVDDDESSTDNYGTVIGIDLGTTYSCVGVM
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAAKNQASSNVNNTVFDIKRLIGLKYNDDTVQKEL
KHLPHYKIENKGNKPVVKVEYQGEETFSPEEISSMVLGKMKSIAEDYLGKKVTHAVVTVPAYFNDA
QRQATKDAGTIAGLNLVRIVNEPTAAAIAYGLDKGDQEKQIIVYDLGGGTFDVSLLSIEGGVFVFL
ATAGDTHLGGEDFDKIVRYLAKQFKKHNIDITANSKAI SKLKREA EKAKRITLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDGGVKKS DIDDIVLVGGSTRI PKVQELLE
FFDGKKASKGINPDEAVAYGA AVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNNRLGKFELTGIPPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAKEYAQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDATAEEFEEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDSDDEFDDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
501..1343 (SEQ ID NO 379)

GCCCCATGGTGACAGAAAAGTATTGATCCAGGTTTCTTTGAAGGTTTGTAAATACGTTTTAACTTG
TGACCTAACTCATTTTCATAAAATCTTGATATAAAATTGGTTTTCTTTGAATTGTTTGTAAATCTCTT
AAGATTGTCTCGTCTTCAGTGTTCGAGTGAGCTGCTATTGCCAGTCGGCGGCATAACAGCAGGT
TCTGGTATGTCATCTTCATCTACTAAGCCGGACAATCCCAAAGCCGCTCTTGTCTTTTATCTCTT
CTAAGGAATGCTTTATGTAGTTCTGACATCTTGCGTAAAGGAAGTACAGTATTAAAGCTCGAAA
CTCAATTGCAACAAAAGTCTTAATTTTTCTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA
AGATACAGAGGAGAAAGGAGGGCCTTAGGCTGACAGAAAAAAAATTTAGTACCTGCCACACCAG
TAGCTCCAAACCCATATATGATTTGATAGAGTTGAAGTATGCTGACAGATCTTACTTCACACTTTC
AGTACATGGCTATAAGCTTGTTTGTGGTTACAAAGCCTTACTAAATAATGAGACACCAGTGTCAT
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTTGGGGAACAAAACTGAGTATTG

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
AGTTGGGCATCAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTCGGAGGAAATGGTACCATTT
TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATTCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACATTACGAAATTTTATATTCAACAAAATGAGTCGGCACCAAAATCCAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTCAAAGG
ATGAATTTATAGAGTTTTACGGAAATGAAAAGAGTGCATATTTACGATGGGAAGATTTTTGAAATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAATAATTGAATTTACAACTTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAAATATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFQYMAISLFGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVEPCIMCASYLRQLGIKKVIFGCGNDRFGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQNESAPNPKIKNTDIESKEYPENQFCSISKDEFIEFYGNERNVH
IYDGKIFEITPLQNKGYDIKELISLDMMQKVPFLEDELGQITDEQIIEFHNLFNINDDGTVNYKK
PIGKYNKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;
CDS: 501..>1502 (SEQ ID NO 381)

CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC
AACTTTTTTCATTTGATTGGGTATTACATATTTTATTTAATTTAGCATTTGTAGTATCAATTATTG
TTAAATTTGTCATGGCTCGATCAAGTTGTAAATTACCCATGGATAAATCTGCTTGAGATTTATTTA
ATTGATTATCCATTTCAAGTAGGACTTTTTGTAAATGCTTCTTGATTCATGATTAAATGAGACGAGT
GTGTGTGTATGGCGCATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG
AAAAATATACAATCTATAATCAGTATGTTTCAAGTTTGAATGGAAGCCCCAAGAAGAACAACAGGG
AAATTAATAAATAAAGGTGTTGGAGAAAAAATAAATTGAACAGAAAGATTCATCCTTTTAGA
TCAAACGAAATATATCTTACCATCCCCCCCCCTCCAAATGCTTAGATTTACTAGGACTACTGCTT
GGAAATTAAGATCTATTCCAATTGCCACTATTCAATATAGACAATTTACTTATTCCACTATATGTT
ATCAATTAATAAACCTTACTCCATCTTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
AACTAATAGATTAGCTAAAACCTGGTACTAGATTTTGGAAAAAAGGTGAAGTTAAATTCAATAATG
AACTCAAAAAATATGAATTTCAATTAGATGGGAAACTCTACGCACACCACTTGGATTCCCATTAG
AATTACCAATCAATAAATAAACAATTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA
TTAAAGTGAAATCAAGTACTTTACCATTAAACAGCTTTAGCCACTAGAGCTATAGATTTGAGTCAAC
AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTTGGAAGATATTAAATTAC
AAATGTTAAGATATCTTGATACTGATACTTGTCTTATATTTGCTACCAACAAAGAATGTGATGGTA
AATTAAGAAAAAGACAAGAAGAAATTTATCGTCCATTAATTAATGAATTTAATGAATTTTTCACAA
TTTATGCTCATAATAAAAAATTTAATCCCTCGACAAAAATCTATTGAATTGAATATTTAGATTGTG
AACTGATGGATTAAGAGGTAATAAACAAGATGAAACCACTCAATTAGTTGTATTGGATTGGTTAA
ATCAATTACCAATTTATGATTTAATTGCCTTGGAGAAAAACAATCTTAATACTAAATCATTTTAT
GTGAATTACTTTATTAAGATCAAATGTTAATGATATTGAACTTTAAAAGAATTATATCAATTTA
ATAAAAAATTCCATTGATGAAGATTATTATCATAAACTTTAGAAGAATTAGTTGAATTAGGAAATT
TAGAACTATTTATCAAACCTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFTRTTAWKLRSIPIATIQYRQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KKGEVKFNNETQKYEIQLDGKTLRTPLELPINKKQLAYLIAHEWTHLPDIKVKSSSTLPLTAL
ATRAIDLSSQOHLSDMKTEKAEMLALEDIKLQMLRYLDTDTCLIFATNKECDGKLKRQEIEYRPL
INEFNEFFTIIYAHNKNLIPROKSIELKYLDCETDGLRGNKQDETTQLVVDLWNLQPLIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKELYQFNKNSIDEDYHKTLEELVELGNLETIYQTEEWGEV
EDTH

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoSeq:
453..3413; CDS: 501..3686 (SEQ ID NO 383)

TATTTATATATAATCTAACAACAAGTACTATCCCTTAACCTATTAGCTCAATGTCAATTCCTTCATTA
AACAAGAGATATGGTAATTGTTGATTAGACAACAGTTGGGTATCCATTTGTATTGGAACGCTTTTT

TTAAACTGCTGTTTTATTGTAAAAATTATTGTGCTCTTTCTTCATAACATTATTTGTAACAGTCTC
TAACTGTATTGTTGGGCTGACAGTAGAGTATTGCGGTCATTTTATAGGAGTGATTATAATTCTCTGT
GAGAAACGCAAGCAACAAAAAGAACAAGGAAACACAATCATGATTAATTATATTAATAGTAGA
AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAACAACATCATCCAAAGTTTAA
CAAAGTATTCCTTTTTTTTTTTTCAATTTTACAACCAAAGATAAATAACTACACAACACCAACATTA
CAGCCAAAACCATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT
CGGGTGATACCAGTAGCACACCAATGGCCAACAATAATCCCACTAATGACAGCACAATCTCCTCTC
AGAACCATTCTAAAACTGGCTTGAGAAAACACCAACAACAACACTACCACCAACACCTGCACCTGC
AAATGCATTCTCATTACAGCAGTCACCTTATATTAATCAATTGGAATACTTTACCAATAACCAGT
TTTCACGCTCTTTCAATAGTTTAAATTTTGGAGGATGCCAATGATGCCAACACCAACAATAGTTCAA
CAACAACCTTAAATAAGAAAACCATTAACAAGTACCACCATTCATATCAAGCAGGACTTATTA
ACGATAGTATCGACAGCTTTCTTGATACTCCAACGGAACGATAGAAGATGGAGACGTCAACA
CAACAGACGACGATCAGGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGACAGTACACCC
CAACTTTGAATATCTTGAAATCCAAAAAGTCGATAGCTTCAATATTATATCTAGCAAGCATAGAA
AGAGCAATAGTCAGATTACCTACAATCTGCACGTACGGAAGCCATCCGAAGAAGATACGTCATCAT
CGATGGCTACAATAAGGTTATCTAACAACCTACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA
ATTTATCTATTGATTCCAATTTGAAAACGGTTGATGGAGGTAAAAATCCCGATGAAATAGATGACA
TTAGTTTGAACGAAATAGATGTTGTCAGTGGCACCTAACGATTTTTCATCACCCTATCAGCAAGAA
AGCCGGACATATTTGCTGCTATAACTGCAGCAACGGGAATTCCAATAATCAATTTAAAGGCCAC
ACAAGTTGGTTAGTCAATCGCCTTCCCCGTCTGTCAAAGAATAAGTTTCGCATATCATCATCAACCA
CATCTTCGCCACAGTCTAACTTGCATTACCTTCCAAGTTGGGACTGAAAGGATTCAAATGTTTA
AAAATGCAATAGAGACGCGATAATGTCTGTCAGCAGAGTTATGACTCCAGAAAACCGAAAATGG
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CAATGGCTGTCCTCATCACTCAACCTCCTTCATCATCTACACTGAATTCAAACAACGGCAGCAATAA
CATCTACAAGTCCAGCAGCTGATGAGCATTATGATATTGACAATGACTGTGACAGTCCGTCAAAAA
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CAAATCATGCTAGAAAATCTAGTAATCCAATACCATAACCTCCGACCGAACCCTACCGACAAATA
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GTCCCTTATTTGATGATAAAGAGAATAAAGCTTCTTATCAGTTTGTAAACCATTGCAAACAGCTT
TCAATTCCTCGGGGTTGGTCAAAAAGAATAGCATAAGTGGTCTGCTGGACAGGAAACTACCTCCAG
AAACACCAATCAAAAGAAATCCATTAATGATTTTAAATACCAACAAAGTTGTACCTCCATATAGCA
GTGGATTGTCTGAAGGAAAAGATGTAATGGGTGATCAACATGATATATATTCCTATATTCATGTCT
AAAATCAACGTTTTCTTGGCAGCGTGAATCCCAACACTACTACGAACAACAACACTCAACAGC
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TCAATAACACAAGTTATATCAAAATTTTCCCTTCTTCGGAATTGAAAAAGGAGCAGGTGCTTCAGC
GACCACAAGAAGATTTAGAATTAGTTTTCAATTCTGACATTGAACTAGATGATAACATAATACCAG
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TAGATAAATCAAATGCAACTAAACGAGAAATTAGCGAACCACCTTCAACACCAATCAATATGTCAT
TTGCAAGAATAGTTTTAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCCTGATAGTATAA
TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTTATCCTTCAA
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TTGAGGCCTGGGATTTTAATAATTACTACTATATAATGACAGAATTCTGTGAAGGTGGTACATTAT
TTGATTTCTTAGAGGAAAATAAACATTACAAAATTGATGAATTTAGAATTTGGAAGATCCTAATTG
AAATTCTAAATGGGTTAAAATTTATTCATCTGAAAAATTTATTACATTTGGATTTAAAACAGCAA
ACATTTTTATCACTTTTGAAGGGTCATTGAAAATTGGTGATTTTCGATTGGCTACTAAATTGCCTA
TACTAGAAAAGGACTTTGATCTTGAAGGAGATCGTAATTATATTGCCCCGGAATTGATTAATGACA
AAATTTTATACTCCGTTTGCAGATATTTTCAGTCTTGATTGATTATATTGGAGATCGCTGCTAATA
TAATTTTACCAGATAATGGAACGCCATGGCGTAAATTGAGAAGTGAGACTTGAGTGATGCTGGCC
GATTATCAAGTGATAATATTTCAATGTTTTTACAACACAATCCAAATACCAATAGCAATATCAGTG
GCAGTGGAAGTAGAAGTGGTAGTGCGAGTACAGGAGGCAATGGTAGTGCTGGTGATTGA

MDSNPCQDVSGDTSSTPMANNNTNDSTISSQNHSKTGLRKHQQQHYHQHSHSQMHSQSQQSPYIN
QLEYFTNNQFSRSFNSLILEDANDANTNNSSSTTLNKKKTINKSPFFNIKQDLLNDSIDTFLDNSNT
ETIEDGDVTTTDDDDHDFDDEDIEDPEAVQYTPTLNLSKSKVDSFNIISSKHRKSNSQITYNSHVR
KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSDSNLKTVDGGKIPDEIDDISLNEIDVAVAPN
DFSSPLSARKPDIFAAITAANGNSNNOFKRPHKLVSQSPSPSSKNKFRISSTTSSPQSNLHSPSK
LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSKIFGKSAKIRRAYTPHTSTPMAVSSLNPPSSS
TSNSTTAAITSTSPAADDEHYDIDNDCDSPSKNRKSSNISASSIIYQDENHIKSNHARKSSNPIPY
PPTEPLPTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS
GSSDRKLPPEPTPIKRNPLMILNTNKVVPYSSGFAEGKDVMDQHDYSHIPQONQRFPGSVNPNT
TTNNNNTQQHHSDLSIEVGRNNSYDASSSTINNTSYIKIFPSSELKKEQVLQRPQEDLELVFNSD
IELDDNIIIPETPTKKSLLPNQHHQHHLPLYTQSKSPLLKFDTEKDGRRLNSIVLDKSNATKREISE
PPSTPINMSFAKNSFKKPMNNAERGDDPDIIAQRIDIMPSLDEVDSVSVYPSKIDEHLIEKFGMK
NIKYIGSGAFSIAFECLFNNEKFAIKRTKKPLIGKLEKQTIKREIEALRVLTSIKEDEATNMQEQE
EGKEYLVYFIEAWDFNNYYYIMTEFCEGGTLDFLEENKHYKIDEFRIWKILIEILNGLKFIHKN
YLHLDLKPANIFITFEGSLKIGDFGLATKLPILEKDFDLEGDRNYIAPELINDKIYTPFADIFSLG
LIILEIAANIILPDNGTPWRKLRSGDLSAGRLSSDNISMFLQHNPNNTNSNISGSGSRSGSGSTGG
NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:
501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAGACTTGCTTTTACCAGTTTTTTC
AGCATTTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT
TGATAAAAAGAAACCGTGAAAAGGAAGTATTGTGAAAAATCGATTGATATTTTTTTTTTCTCCTCCT
TCCTCACTGTAAACAGTAGTAAACACACTAGTTACAACCTGATGACCTGCATATTATAAATCTTCTG
AAAAAATTTTTTCCCTGTATTTTTGTAAATCTTCTCGCTCTTCTCACTCACTCACACTTATTAAT
GAATGAAAGGTTTGGTGTCTACAACTCCACTAACAAATCTCACTCCTGTGCCTAAACACACACA
GACCCACACGCAAACCTTTCTCTCAGAAACAGAAAAAAATTTCAAGCAAAAATTTTTCCATC
TAGATTTTTCTTCTCAGAATATCAAGTAACTTTAAAGATGCCTGTATGTACAATAACAGTGTTAT
AATGATGTCTTTCAGTCTTTTATTGGGTGATTATTATAATAAATGGCAGATGAGAAATATATTGGA
TAATAAACCTTGCAAATGAAATCAGTTGACCATTTTGAAATAATGGACCATTAGCAATACCCAGAT
TGCTGGAACAAAGACGAGAGAACTAGACAACCTCAGATATAATAGAACATCCATACTAACTTCACTC
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GACCATTGCCCAATGGATCAGATTGGAACCTGACAACAAATCAGATACAATGCTAAAAGAAGAC
ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W_homolog 51aa (SEQ ID NO 386)
MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNAKRRHWRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ
ID NO 387)
GATTTTCATTTGCAAGGTTTATTATCCAATATATTTCTCATCTGCCATTTATTATAATAATCACCCA
ATAAAAGACTGAAAGACATCATTATAACACTGTTATTGTACATACAGGCATCTTTAAAGTTACTTG
ATATTCTGAAGAAAGAAAATCTAGATGGAAAAATTTTTGCTTGAAATTTTTTTTTTCTGTTTCTG
AGAGAAAGGTTTGGGTGTGGGTCTGTGTGTGTTAGGCACAGGAGTGAGATTTTGTAGTGGAGTT
TGTAAGACACCAAACCTTTCAATTAATAAGTGTGAGTGAGTGAGAAAGAGCGAAAAGAAATTACAA
AAATACAGGGAAAAAATTTTTTCAGAAAGATTTATAATATGCAGGTCATCAGTTGTAAGTGTG
GTTTACTACTGTTACAGTGAGGAAGGAGGAAAAAATAATCAATCGATTTTTCACAACTACTC
CTTTTCACGGTTTCTTTTTATCAACAGACAATTCAACCATGACTAGAACCTCCGTCTTAGCTGATG
CTTTAAACGCCATCAACAATGCTGAAAAAAGTAAAGACAAGTCTTAATCAGACCATCCTCCA
AAGTCATCATAAAATTTCTTGACTGTGATGCAAAAACACGGTTACATTGGTGAATTCGAATACATTG
ATGATCACAGATCCGGTAAAAATTTGTTGTTCAATTAAATGGTAGATTAAACAAATGTGGTGTGATTC
AACCAAGATTCAACGTCAAAATCAACGACATTGAAAGATGGACTGACAACCTGTTGCCAGCTAGAC
AATTCGGTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC
ACGTTTCTGGTAAATCTTAGGTTTCTGTTTACTAG

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLTVMQKHGYIGEFEYIDDHRSKGIVVQLN
GRLNKCQVIQPRFNVKINDIERWTDNLLPARQFGYVILTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
3042..3259; CDS: 501..4616 (SEQ ID NO 389)

CAACGACAACAACAATAAGAAGAATCTTTTCCAGATATTGTAAAATCCTTATATTAAATGTTAATA
GAAGCCTAAAAATTGCTTGAATTGATAGATTGCTGATTCTTTTGCTAGAAACACGCGTTATATTA
CTTATCCTTTCTGTAATTTCTTGATCTCTGTTGAATCAACAACGCCTTTGTTTCTCTTTCTGCC
TCCCTCTGCCACCCCAAGTTTATTTGTTTGCTTGTGCGACGTGCTGCCAAAAAAAATTTGAGTTC
TCTCTCTCTTTTACAACAGAGAAGAGACAAAGAAAAAAAACATCAAAATTAAGATTCAAGC
TTTTTTTTTAGTTTTTTTAAACAACAAAATTGAAATTACAATCCTTGAATTTACAATTCATATTC
AGCTCTAAATACTAATAATTATAACAATAATTGAATTGAATTATTCTATAAACCACTGATATTGAT
TTTATCTTTTTATTTTTGTTTGTCCATAATTGTGTCATGCCTGACAATATAGAAGATCGATCCG
AGATACCTTCTGATGCAAAGGAAATTGTGACTACAAATGAAATTGAAGCAACAGATTCAAGACATA
CAACAAATGTGCGATAATGAACCTCCCTCAAGGTGAATCCAATGAACAAACAGGAGATGACTCAAATG
ACAACCTTGCATCCAAACGTCAATTAATCAATGATTTATTACACAATGATCATTTTGAAGAAGGAA
CAGAACGTTACATCATCCCTCAAAATTTCTTACATGAATTTTGAATTTACCAATCGATAATTTTA
GTGATTTGAAAGATCAACTTGGTCTTATTTGATTTCCACTCATTACTTAATGAACAAGGTAATTTAT
ATCCCGAGAATGAAGAACCAGTCACTTTTGTCTGATCGCCAGAAGTATTCAACATTTGGGTG
AATGGTTTGAATATTGGGCCAACCAATTATTAGAGCTATCATTATTAATCCAGACACCAAGAAA
AACAGATTGAAAGATTCCCGCCATTATTTTGGGTTCATCAATTAGGTAAAAAGACGCAACCAACAT
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TACCAGTATTGCTTTCCAAAACAAGCACTTTTCATAGATTAAATGGATGTTATACGTTATAATGTTT
TTAAAGCACCACGAAAATCGACGAAAGATTTTAGGATTTGGTTTATTGTCCCAAGATAAAGGCT
TACAGTATTTGATTTCAATACAACTTTTATGTTTGAATATCTCCAAAAAACTTTGGTTTCACCAA
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YJL198W_homolog 896aa (SEQ ID NO 392)

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CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCVKCKTPGTDPMDATKASQYIFGTMWNSTIMIL
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YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
501..2276 (SEQ ID NO 393)

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YJR049C_homolog 592aa (SEQ ID NO 394)

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RATAWCSFDGKVRTELKKGYVVTIQASPFPLPTVMSSKTEYIDSVSRNLHWNIREQQKPFSSYLKP
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YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)

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YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
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IKESSYVNIPVIALTDMQSPSEYVDVAIPCNNGKHKCIGLIWWLLAREVLRLRGIIPDRTEWSVM
PDLFYFRDPEEIEQNAVEEAKTEGVEGAPVAEAEETEWTEGETEDVDWADSGATPSC

YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)
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YLR088W_homolog 444aa (SEQ ID NO 398)
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YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO
399)
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YLR167W_homolog 229aa (SEQ ID NO 400)

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YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

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CTTATGGTACATGTCAATTTCCCGACATTGGGGTTTGTGTTGATCGATACAAACGAGTCAAGAGTT
TTACACCGGAACCATTTCTGGTATATTGAGATTGAACTAGGAAAGAGAATAAAAAAGACAATTTTCA
ATTGGGTTCGAGGTCATTTTTTCGACAAGATGTATGTGGTTATGCTTTATGATCGATGCTGCAAAA
GTGGAGAATTTGGAACCATATCAAAAAATAGAATCAAAACGGAAACCAAATTTCCGTCCATTCCCAT
TGACAACCGTGAGTTACAAAAGATTGTGCTAGATTTTTTAAGATGTCTGCTAAGACGGCGTTGG
CAGCTGCTGAAAGACTTTATAACCTAGGGTATTTGTCTGATCCTAGAACTGAACTGACAGGTTTG
CCAAAGAAACCGATTTCAAGAGCTTACTAGAGGTGCACAAACAAGATCCGCGATGGGGAAGCTATA
CAACAAAGCTTTTGAACGAAGGTTTCGAAACTCCTCGAAGCGGTTCTCATGATGATAAGGCGCATC
CTCCAATCCATCCTATCAAATATGTTTCTTTGGACACCCTAAACACCCTCGATGAAAAGAAAGTGT
ATGAATACGTTGTGCGACGCTTTATTGCCTGTTGCTCCAAAGATGCTGTTGGTACGCAACCGTGG
TGACTTTAAATGGGGAGATGAATTCCTCACCGCAAGTGGATTAAATGGTGCATGAAAAAATTTATT
TGGAAGTGTATACTTACAAAAAATGGGAAAGCTCTAAACAACCTACCGAAATTTACAGAGGGAGAAC
AGGTCAAGTTGTCGAGTGGAATATTGAAAGACGGTAAACAAGTCCACCCAATCATATGACCGAGC
CCGAGCTAATTGCATTGATGGATGCCAACGGTATTGGAACCGATGCTACTATCGCTGAACATATTA
ACAAAATAGAGACTAGGCATATATTAATAAATTGAAAAAGGGGAAAAATGAATATATTCTTCTTA
CTCCTTTAGGAATGGGGCTTATAGAAGGCCCTTGAAAAAATGGAATTTGAAGATGTATCACTATCGA
AACCATTTTTGCGGAAGTCGTTGGAACGATCACTTGAGGACATAGCAACCGGGTCCCGGCCAAAAG
TGGATGTTTTGAATACAACAATAGGCGTATATGTTGACGCTTATAGTGTGTTGTTCTCATCAGATAC
TTGTTTTGTGCAATGAATGTAGGAGAATTATACCTTGGAATAGCAGTAACAACAACAACAATA
ATAATAATACGTAA

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKNYDFTFTFNSDGPQVMTTSVAGHITGLD
FGSAFSWGNVCVPGRLFEADIKTIITKKSIIYENIAEEARNADKLMIWTD CDREGEYIGFEIMNAARK
YNRNLGLNNIWRARFSLERNHIIIRAAKNPVNLDMSAVSAVSCRMEIDLVRVGSFTRLLTDQLRQK
GII EKNELASVGTCTQFPTLGFVVDYRKRVKSFTPEPFWYIEIETRKENKKTIFNWVRGHFFDKMYV
VMLYDRCKKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAERLYNLGYLS
YPRTE TDRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT
LNTLDEKKVYEVVRRFIACCSKDAVGTQTVVTLKWGDEFFTASGLMVHEKNYLEVYTYKKWESSK
QLPKFTEGEQVKLSSGILKDGTSPPNHMTPELIALMDANGIGTDATIAEHINKIETRHYINKLK
KGKNEYILPTPLGMGLIEGLEKMEFEDVSLSKPFLRKSLSLEDIATGSRPKVDVLTNTTIGVYVD
AYSVC SHQILVLCNECRRIILGNSSNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:
828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTAATACTAAATTAGAGGTTACATTAATACAACCTTAAC
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ATTGCCTTATATACAGCTTGTAACAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC
CTATTGTAAGAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG
TAACGACAACAACATAACAACAAAAAACATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
CACACGATAAGATTTATCAGTTTCTCTTCTCGGTTGACCTTAATCTGTTTTGTATAGACTTTAT
TTTTTTTGTTTTTTGACCACACCCACTTTTAAATATACAAAGATATTTAACTGATTATAGAAAACA
CAACAATAACCCAAATACGTTAACCACTTTTATTACATATGATAGACAATATAATCAATAATTTGC
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ATTCTGCTCGTGTAGCAGATATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC
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GTCTACATTCGACCTCAAGAAGGAATTTACCTGAATTGCCTTCAAATTCATTATTTGGTTGGATTC
CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGAACATGCTGGATTAGATGCAGTTGTGTTTT
TGGAATTTTTTAAATGTGCAATTCGAATAATAAGCATATGTTTAGTATTTGCCATTATTTATCATAT
CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATATGACAACG
ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTGCTGGAATTC
TGGTGGCAAGTAAATAACGATGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA
CCTATGTATTTACATTTGTTACTGTTTACTTTCTATTCAAACAAACCAATAGGATTATTTCTATGC
GTCAGAAGTATCTTGGATCGCAAAATTCAGTCACCGATAGAACGGTAAATAATCTGGGATACCAG
TACAGTTTACAGAAATGAGTGGCACTCGCACGGCACATTGACCGTTGAATATTTGGTGAAGTGGATT
CTGTGTTGATTGTCAAGGAGTGGCAAAATCTAAACAAACTATTCAAAAGAAGGAGAAGAATAGTTC
GAAAATTAGAGGAAAGTTGGGTGAATATTTTGAATAAATGGGATAACCAATAAGAGCGATTGTA
TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG
AATCACCAGACTGGGGATCTCAAAATTCGAACCTCTGCACAAGCTTCAATAATAGATCAAGACTCAG
AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATCGCTTGTGTAATGATGAACCTGAGAACAAGAC
CAAGTCTTCGGAAAGGTTGGTTCGGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG
ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAACTAGAGAATATCCCGCCACTTCGA
CTGCATTTCTCACTATGAAAACCGTGGCTGAAGCACAAATGTTGGCACAGGCAGTCTTGGATCCAA
AAGTCAATCATCTTATCACCAACTTGGCCCCGTGCTCCTCATGATATCCGATGGGATAAATTTGTCA
TAACTAGACAAGACAGAAATACAAAGATCCTTGCTGTCACGATATTTATTGGTATAATGAGTTTGT
TGTTGGTTTATCCAGTCAGATTTATGGCTAGTTTTTTAAACACTAAAAGCATTTCTAAAATATGGC
CATCATTTGGGAAAGCTATTGAATCGCATAAATGGGCCGAAACTTTGATTACTGGATTATTGCCAA
CTTATTTATTTACAATTTTAAATATTGTGATTCGGTTTTTTTATGTATGGATTCTGAAAAGCAAG
GTTATTTATCTCATAGTGATGAAGAGTTGTCATCGGTATCCAAGAAGCTTTTCTATATATTTGTGA
ACTTATTTTGGTTTTTCAAACTTTTGGTACCGCCTCTTTTGTGATACGACCAAAATATGCATTTG
ATTTAGCAAGATCACTCAGAGATTGTCAATGTTCTATGTTGACTTAATAATTTACAAGGATTGG
GTATATTTCCATTCAAATTATTATTGGTGGGGAACCTTACTTCGCTTTTTAGTGAATTCATTATTTA
GGTGAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT
TACCACAACCAATATTGATATTTATTATTACGTTGGTATACTCGGTAATGTCTTCCAAGATATTAA
CTGCAGGGTTACTATATTTTATTATTGGTTATTTTGTGAGCAATAACCAATTGCTTTATGCTTGTG
TTCATCCCTTCAACATCAACGGGCAAGTTGGCAATAATTTTCCAAGAATCATATTAGGGTTAT
TCTTTTTTCAAATCACAAATGGTTGGCAGATTAGCAATTAAGATGCAATCACATGTGCTACTTTCT
TGGCACCATTTGCCGTTTTTGTACACTTTACTTTTTGGTGGAGTTTCCATAAACAATATATCCCTTGT

CAACATTTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA
TCATTGAAAACAACAATAATAAACTCTTGACGAAAGAAGGGAATTGAACACTAAATACGAATACC
CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA
ATCGAGATGGTACAACCTGTACGGAAACCACCTCAATATTTTCAGTTCAGAATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLOIILQONDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNFSLHSTSRRNLPPELPSNSLFGWIPTVYKITEQEILEHAGLDAVVFLEFFKMCIRIISI
CLVFAIIIIISPIRYKFTGRVDEDYPDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLYTIFTYVFTFVTYVFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRNLIGEVDVSVLIVKEWQNLNKLFRRRRIVRKLEESWVEYFEKNGITNKS DLI SLHPQVGESYRF
SNRYTDDAEESPDWGSQNSNSAQASI IDQDSESVEGDSSDTLNRLLNDESRTSPSLRKGWFLGFGP
KVDSINYTDTKLEVIDKEITRARTREYPATSTAFITMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWP SLGKAIESHKWA
ETLITGLLPTYLFTILNIVIPFFYVWISEKQGYLSHSDEELSSVSKNFFYIFVNLFLVFTTFTGTAS
FVDTTKIAFDLARSRLRDL SMFYVDLI ILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFGLQLPQPILIFIITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPHSTGKVPWI
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGTTVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq:
948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT
TTTGTTTTATCTTGAGAACCTGTGTTGTTGTTGGCGTTCTATCTCTTTATATATTTTCTCTATTA
ATTCAATTGAACATTTTGAAGAAATCTTTCTTAAAGCATCTAGTGACACATGATCTCTAATCT
CCAGTCTTTTGATTAAATATTCCTTTTAGAATATCAGGTGAAGAAGTGTTGGTAGTCATAGCTAGTA
GATACTGTGTGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCAGTGTATATT
TTTCTTTTGTCAATTCCATCTTTTTTTTTTTTCTCTTGAGAAATGTATAACAGAGGATCCATCCATT
TGCTTGACAGAGAAATACAGAACACTAAACAAACATTTTTTCATTCCCTTTCTTGTTTTGTTCTGTT
ATACCCCAAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAAATTGACAGCAG
ACATAGCAAGCTCTTGCAACTAGTTTCCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA
TTAATGTTGCACCAACTGGTCGACAAGCCAAAGACATATTCAACAGATTAATTACTCCGAAGAGT
TTGGAGATGACCTTGATTTTGATGAATTTCCCATCTTCGACACCCGGTACTAGAGAAATGAAA
ATAAAGCTCAAATAGAAGCACAAAGATATTCTCTTGCGAAAAACACACCAACGCCCAAGAGAATCT
TAGAAAAACCGGTGTTATCTGAGTTGGTTGAAAAACAGTGGTGCTTATTCCTATCAAATAATGA
TTGAGAATTTGAACACAAACCAAAAGTTGATTGATTCCTTTATGTGGAACTTGAATGAAAGCTTGA
TTACACCAACTGAGTTTGCAGGAAATTGTTTGCAGTGATTTAGATTTACCATTACAGTATGGCTGCAC
AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACAACCTACCAA
ATAAGGGCCCTTACAATGTTACCATTGATTTTATCAGTAAACTTAAATAACAATTTATACCAAGATA
GATTTGAATGGGATATGAATCAAATGAAGTTACACCAGAAATTTTGTGCTGAAATAGTTGTTGCTG
ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG
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TAATGTTTGAACAAGGAATTAGAATTTTCACTGAAAACAGTGTTCAAAATGGAAATGACCGTTGGG
AACCTTTGGTCAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAATGAAAGGGTTAGAACT
TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG
GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSFPKRLANDSDNSLLINVAPTGRQAKRHIQQINYSSEFGDDLDFDEFPS
TPGTRSLNENKAQIEAQRYSLAKNTPTPKRILEKPVLSSELVEKPVVLIPIKIMIENLNTNQKLIDS
FMWNLNESLITPTEFAEIVCSLDLPLFSMAAQIADSINQQIEEYSYASNLQLPNKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIRVKKEVIDGTFDNE
MHNHLVKGIMFEQGIRIFTENSQVQNGNDRWEPLVEVLTSSEIERRENERVRNLRRLKRENMRRDY
DDHSRRRQAGKRRYDELEGAWV

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
TCGCTCCTGACCATTGTTTACTATATTCAACAAAACGAATTCAACAAGGCAAACGAAAGCTACATG
AAACTAAGTATCGGCAACGTCTGTTGGCCAATTGGGGTGGTCAATGTAGGTATTCATGCAAGAAGT
GCAGCACTGAAAATAACCGGTGCCTCTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG
TTTAGTAATTTTTTTCGAGTTAGGGCTATAGCCCTAAGACATTCACACAACCTAACAAAAAGGAAGT
TCTCACGCACATAACGTGTAACCCACATAAAGAAAGAAAAAAAATTTCCTTTGAAAAAATTCACA
TCACGCTTTAACCACCTCAACCTATAACAACCTCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTCGAATTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACGGTAAAAAATTCAAACAAACCAATTCAGGTCAAGGTTCAAGATACCAATACACTT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA
CCAACCTGTAA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNKVNANGKKFKQTKFKVGRSRYQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron
1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGGAGCTAATTATACCCTCATT
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TTTTTTTTTGGCAATATAGAGAAGACTGTAATAAGTATAGCTCACTAAAAGTCTTTTTTTTTTCTATT
CGTTTTATATTTTTTTAAGAAATTTGATGTTGATTTGGTAAATGCCAAATTTTAAATGTGTGTTAG
GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTTACGCACAGTTTGTCTTA
CCAAATACATTATATATATATATTTTTTTTTTTTTTTGAGTAGAGGAGCTACACTAGACCACAGTGC
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CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT
AGATATTCAATTAGATATGGAGAAAGGAAGATAAAAGGAAAAAGAAAAAAAAGAAAGAAATAA
AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACAACCATTAAGAATTAAGTTTAAATAC
AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAAACCATTGACTGAAGTACTACACCAAGAAAGGTA
TAATGATTTACGATTTTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAAGAAATA
CAATTTGGGGATATTGATGAAATTTATGTATAGGAGATTCCATTTTCAAACCTGTGTAATGGAAAA
CTTGAAAAATCAAATCAAATCAAATCATAACCCTTCAATATATTCCTTCCTTATCTTACTTTTCCT
ATTAAACAAAGACTAAGAAACATTCAGTAAATACTAACAAAAATTCATTTATATAGACGTTTC
TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGTTCTTTT
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TGATGAAGTTTTAGTTGTTAGAGGTTCTAAAAAGGTTCTGAAGGTAAAGTTAATTCTGTTTATAG
ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGTCTCTGTTCCAAT
CAACATTCATCCATCTAAAGTTGTCAATTACTAAATTACATTTGGACAAAGATAGAAAAGCTTTGAT
TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRKARKAYFTASSVERRVLLSAPLSKELRQQYNVKSLEPIRQNDVLLVVRGSKKGS
EGKVN SVYRLKF AIQVDKLQKEKSNGASVPINIHPSKV VITKLHLDKDRKALIQRKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

TTCATCTTTCGAAATCTTCCCTCTTGGAAACGACCAAGAGTTGGATTCCGTGCCCTTGACTAGCAC
AACTTTGTTCAAATCTTTATTGAATAATGCAACACCACGAACCGGTATGGTCGATTTATATTTTCC
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TGTAAGTGAACGTCTTCATCTTCATGCTTTGCAATCGGGATTCAACTGACGAACAAAGTCAGCATA
AAACCATGTGCTTCCCTCAATCTGAAACATTATCTTTCAATGGAAGATAAATCCTCTTCGGGAAC
ATTCACCACAAATCTAACCTAACAATCTTCCAACCCGATCTAGAGTTTGATTAGCTAAACCAT
GCGTAATTGGATCGACATATCTTGTTATTTTCTATGATTAATCTTTCTTTTCTTTTCTTTTCTCAC

MFVYWINNLCEIIQCICWRRRRQGRTEFFPSYFFSLSLFFQSHCSSVKGWLFC AEPCGSVNARHRV
IFGETKRILKNRGLNSTTDWLDDKMOSVFIRTFATSRIEFQRYQPRFVNTIKETVKS AQEKSYSIT
RPLGLSKPVLLNHKLSDTYSLSNIYEELFGQKSKERRQKQLDYDLKHSP IYEVKSFENTKGKIFTP
PVSYFRQDKSLYFPDFIAKTLAGNQSRSLYDSLDRNLSIVKLFSSVAGEQCTR SYFKVENKDYYSD
YDTFVEEYPHTQILDVNPMSQWIKGFVTNLSTGNLRKLTLPASRYENYFILPGHIMSAEIREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDKLMMWKVVKGVOREMTK

CCAGTGCCTTTTGGTTTGTTCACATCATACACTTCACTGAAACTAAATAAGTTTGTTTACATTTT
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AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGAAATTGCTGGTGCGCAA
AAAGATTATGTGTATTTTATGTGCGTTGTTATCCTGCACACTAAAATTGAGCAGTGTACACACACA
CATATTGGGCTGTATTTTATTTCTTGTTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT
TGTGTGTGCTGTAATAGTGTGTGTGTTCCAAGTCCCAGCTCTCACAGATACTCACGCACGCCATA
CTACTGAAAATTTCTCTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTTCTTTTACGTT
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TCAAAGCTCCAACCACTTTTGAAGAACAGAAATGTTGGTAAAACTTTGATCAACAGATCTACCGGTT
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TCACCAAAAAGACAACCAAACCAAATCAAGAAAACCTACTTACGCTCAATCCTCTAAATTGAGAGAAG
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AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTTCAATTATTGG
CTTTGCACCGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAGTTTCTTCTGGTTTCAAAGATGTTG
TTTTAGAATCTGTTTAA

MAVGKNKRLSGKGGGLKKKVVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVCLADLQGSSEHSYRKIKLRVDEVQGNLLTNFHGLDFTSDKLRSVLRKWQSLVEANVTVKTSDD
YVLRVFAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNCTLAQLTSKLIPEVIGREIE
KSTQTIFPLQNVHIRKVLLKQPKFDLGSLLALHGEGSTEEKGKKVSSGFKDVLVESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)
TGATATGGATTTTTCAAAACCTAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTGCT
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TATTTTAAATAAAACAATAATAGTAATAAAAAAAAAAACCTTCTTTGCTTTTCGAGAATTTGTAAC
ACATTGTTTCTTTCTTTCCACAGCAACCAAATTTTATTTTATTTTCTTTTGGGACTTACCCACA
GTTGCTCAATTATGTATAACAAGGGTAGAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC
CTTTTCTTTCAACAACGATTGCTATATGACCCCCCCCCCTAAGCATTCAATTGCTTTTATATATATTTA
ATAATGTATTTCTCTTGTTCAGGATAATTATCACTATTTGTGACGTTTAATTTTTTACATTTCTTCT
TCTTCTTCTTCTTATTTCAACATTAAAGAACATTTAATATGTATTTCCCAATCATTGTATGGTTAT
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AATTTTAAAAGAACGTAAAGTTGCATTCAATGATGCCTTGGAGAATCCAAAATTAATTAGTTTGG
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TGAATCCTCCAGATGATTCATTAAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG
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CTTGGTCAGAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA
CAAAGGATCAATTGGTTGAAAAATTAAAGAATTTAGTTATCAAGCCACTCATTCAATTAGAGATT
CCAAAGAATCTTTATTTGATTCATTGGATTTATTTGATAAAACCATTTTGTATAAAAAAGGTCAAA
TTGAAGATGAATTTTTCCAAACTTGGTCATATTCTCAATTACGTGAATGGCTTTATTTACATGGAT
TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCCC
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATACTTGGTTGGCAAACACTGAAAAGAAGTCTC
AACCTTGGATCACAAAGGGAGAACAAAAGTCTCAGAAAAAGAGGGTAGTAATTTGATTAATGATA
CATTTCTTTGTTGGTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)
MYFPIIVWLYVSITFVVANYGFDQWNTDDLKQFLKERKQVAFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNNNLNPDDSLNDYLNFDYLFGRKENYSIKEWIFESWPVTSLQTFLTQNNIQYSAKDTK
DDLINKVKDQFDSISKKNHGSSFPYGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDSDLDFDKTIFDKKGQIEDEFFQTWSYSQLEWLYLHGFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTTEKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417)
ATGAGTTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG
ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAAAATCTGCATAAAGATTAAAGTGAAA
AACAATTTCCGAAAAAAGAAGAAATCGAACACATTAGAAAAAGAAACGAACAAAAGAAAAAAAT
TTCAAATTGTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT
TTTATTTATATCACCTGTCAACAACAAATTTCCAAATAAATACAACTCAGAAAAAACACTTACTAT
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAAACATTCTTGCCTTTTCATCCTTGATTATCATATT
AGATCTTATCTTTAATTTGTTTGAATAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA
ACAACAAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTACCAAAAC
TGAGTTTCAGTCCATTTGATTCACCAGAATTTGTTTCACAGATCATAACTCCCCTTGTAAATACAA
CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTGCGGAATTAGTCAAGACCC
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCTGTTTTTGGGAATGCTCAACATTTT
GTGCTAGTGAAAACCTGTGCTGTTGAAATATTGGAAGATTTCAATTGGAGTCAAGTCACCAATGAAA
GTTTGAACCTTCAGGATTAGGTAAGATTTCAATTACCTGACAAATCATCAATTGATAATTCCATTG
AAACCGAAGAAGTTCAAACCTTGTGAAGATTTAGATTATAGTGAAATAGATGATGACCATCATTGTG
TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTGTATG
TTTGAAGGCTATTTACCTGGAAAAATGTTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG
CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTGTTAGTGGTATGCATG
CTTCAATTGCGATACATTTATCAAGAGAATATTTGAATTTCTGAAACTGGTGAATTTTATCCTAATT
TAAAGGTGTTTATGGAAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTTCAATTATG

CCTTAGTGTCCCAAGCTATAGTTAAATTGAGTGAAATTTTACCATTGAGAGAGTTCATTCAACTGG
GGTATGATGACATTACTCCAGCTCAAAAGCAACATTTATTGGCTAATAATGATGTGCAATCAGTCG
AAGTTTATGATCGTTTGTGTGTAGATGACATTATTCCTAGTTTGGGAAGCAAATGTTGTGTTTAATA
CTTCCAACCTTGTGTGATAATAGCAATTTGAGGGATGAATTTAGATCAAGATTTAGAAACATTTCTG
CCATTATGGATTGTGTTGGTTGTGATAGATGCAGAATGTGGGGGAAAATCCAAACCATTTGGTTATG
GTACCGCTCTCAAGATTTTATTTGAAGATGACAACCTATGATAATCACAATTTGAAATTTAGAAAGAA
TTGAAATTGTTGCCTTGATTAATACTTTTGATCGTTTATCTAAATCTATTGAAAGTATTAATATGT
TTAAAGAAATGTATTTGCAACACCTTAAAGATATTGCTGAAGGATTAACCCAACCTGGTGTTTACG
ACAAAATACAAAACAACAAACCAGGTAACGGATTTGCCTTCCCATTTGTTAGTCCATTACCTCAGA
AAAAACCTGACCAAAACCAACCCCCCAAAAATCAACAACAAAAACAACCTCAAGAACTGACAAAA
AAAGACTTACATTAGAAGAAATTGCCACACAAAACCTGAAGATCGAACTTTTATTGAAGACTTCA
GATTATCCTTTGATGAAGTTTGGCAAGCATTAAAGATTTGTTTAACTAGTTATCAAAGATTCCCAG
CCGTATTGAGTAGATTACATTGGTTCAATTGAATGAATGGTGGAAATAAATTGCTTGGTAACCAA
CAGTTTATGATTACCAAAGTTCCTTTGATGTTGATGCCCTACAATACAGTCAAGTCCTTGGATAA

YML130C_homolog 580aa (SEQ ID NO 418)

MKIFRLFSLLIVQFIINTTVAVSPVSAVLPKSSFSFDSPEFCSQIITPTCNTTFTYIDELNKNDIR
PYLSELVKTSYFRYFKVNLQKCRFVNAQHFCASENCAVEILEDNWSQVTNESLKPSSLGKISLP
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCYVNLVNNPERFTGYGGNQSFVDWKAIYSENCFPN
TNPMSVTNDADNGGEQCIENLFRVVSVMHSAIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIFYNYALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDVESVEVYDRLLLDDIIP
SLEANVVFNTSNLFDNSNLRDEFRRSRFRNISAIMDCVGCDCRMWGKIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEMYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA
FPFVSPLPQKKPDQNTNPKNQKQPOETDKKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPAVLSRFTLVQLNEWNNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq:
508..667; CDS: 501..1001 (SEQ ID NO 419)

TGTGAAAAAAATTTGGTGTGGATGTTGTTGTCGTTGTTGCGTTGTCCACAACAAAAAACAAGT
AACAATTTCAAAGTTGGGCTTGGAGATCGATTTTTCCTCCGCTCTGTGTGGCAGGAGACAATTG
AGTCGACCAGTACGTTTAAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTCCACTT
ATTCTATATCAATGTAAAGTCATTTTGTGATAATATCGTAATTTACACATTTTCGTATATCTCGGCA
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTATTCAATCAGGAGTATAGAA
TTCCACCCAACAACAGATTTTCCGAATGCGAAACGAGGACGACACACAACGACTAAAGAAG
AAGAAGAAAAAAATATAAATAAATTGATCACGCACACATTAGAAACACAATATTGGATCACTTTT
TTCGATAATACTACCACCACACAGCTCATTCCACCTCATGCCCGAAGTTCTACTGCTCAAAAGC
GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA
GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAAATG
GAGTATCCCCAGCAGTATTGACTTTCCTAAAGATTACCCATTATCACCACTACATTAAAGTTTG
ATCCACCATTTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGTATTTTCGATTTTACATCCTC
CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA
AGATCTTGTGAGTGTCATGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG
CTTGTAATTTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT
CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)

MPRSSTAQKRLLEUYQQLSRDPPPGIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAVLTFPKDY
PLSPPTLKFDPLLPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP
NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID
NO 421)

CTACACAAAGCTTCGAGAGTTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGTCTTTTCCTTTATGATTGTTCTTTAACGGAATTGTGTTCTTAAAACAAAATCAGTTCTGC
ACGTGATATAATCTCCTATCGCTAGTAGTAAGTTTAAATTTTTTTGATCAAAGTACACTCATCAG
TCTATTGTCTGATGTTTCGCATACTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGTA

TTGTAAATTACAATTTTTCTATTGGTTAAAATGATAATTGTTAACAAGTCTTTTTTTTCCCCGGGA
TTGAATCCGGAACTACCATTAATTCACCTCATTCTACTCACCCTTACACCCTCACTCACTCAA
ACAATTATATCAACCCAAAAAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAAT
CTAATAAACCATCCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA
GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAAAGATACA
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC
CTACATCACCTCATTTACAAATTTATGAACCACAATTAACCTTGGATCATGTCATCATTTCCATAGAA
TCACTGGTGTTGCTATGGCCGGTGCCTTTTATGCTTTAACTTGTGGATTTGCTGCTACTTCAATTT
TAAATATTCCATTTGATACTACTACTTTAGTATCTGCATTCACCACATTACCAACATTTGCTCAAT
ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG
TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTATAGAAGTGGGTATGCTGTTTTGGCTG
CTACTGCTGCATTGGAAGTTATTTAGCTTTCCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)

MSRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL
TWIMSSFHRITGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPTFAQYGIKAICAYPFVY
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG
TTTGAAGACTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTAAATAAT
TATTTAATCAAACCTTGGTTGTAACCTTATGATTATGGTAGTGATCTAAGAACACAACCTTGCAAAGCA
ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCCTGTTTCTATTAGATTCCCGCTTTTTTTTT
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAACATGCACGTGTATGTTTCTTG
ATTTTCTCACTACTAGTAAAAAAATTTTCTTCCGCTCACTATTACACATACACTCTTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT
TGGTTCCTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAACAGAGAAAGA
AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAATATGGCATT
TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAGCACAGATTATAACAGTCGTAAAGAAAAA
TTTCACTACCAACAACAATAAGAAAGATATCAAAGAGATTGAGTAATCACTACTTACAAGAAACATA
TAACATCATGGAGAGTTAATTTGAAATACGAATGAATATACAAATGAACTATACCCTTTTTATGG
CCATATCAGCTTTCAGAAATATTTAAACAAAAAATAAAATGAAGAATAAACTTGGATATACTAAC
ACATGTATTATAGAGGGTGTCTGTTGTGCTAAGAAAGACTTCAACCAACCAAGCAGATGAAGATT
GATACTAGAACTTGTTCGTATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT
CAATTCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATTCCTTGAGAACCGAA
TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY
TLTDEGVEFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGYRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAAATACTTACTTTTAGGTTACTAACATTATTTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATTTGTTGAAATCACTATCGTGAGGTAAATAACAAC
TACAGAGTTGTCACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAGCAATAGGTCAT
TTATTGCTGTAATCAAGTGTTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAAACATGAAC
TATATCAACTTTAAATGCCCCAATCACGTGATACAGCACATGGGAATTTGCTGATCTTGCTTCCT
TGCACGTACACGGCACATGTACACGACTTTTTTTTTCTAAATATTTTTTTTTTTGTTGTTGTTGTTA
TTAAACAATATTATTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCCTTTGCATATT
TTTTTTTTTTTCTTTTCTGCCAACTTGATCAAATTCGATGCTACATCCTAATAATTCAGTAGTCG
ATATGCTAGCATGGAACATGAATGAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA
AAATATCAAAACAGAATTCAACCAAAACCGATTTTGTGCTGCACGATTGGCTAGTGCGGTTGACG
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATGAGAATAATGATACTGAACCTTGATGATA

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA
GTGTTAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGACTGGTCCTCCCGGAACATCGATAG
CGTTAGGATCGGGCCTTCGATCGCCATCCATACTAGAGGGGGAACAGCTTCAATATTTTCATGACC
CAGTGAGGCAACAACAGTTCAAACCTTCCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTTCAG
TGAATGATAATGACCACCGAAATCTTGTGTACCAAACCTCAACTGAAAGGTTTACTGCTTCACCTT
CGAACAATATTTGGTAATGAAAATATACCTCAATACCAGAAAACCTAGTAGTGTTGCCCACTCAATCA
ATGAAGGATACAATGATGATACATTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT
CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC
CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACGCGCTCTAAAA
GAAATTACAAAACCTCATCCACTTCCCTCAAATTAAGATCAACTACATCAAAACCTTTTCGATAAAA
AAGGGTCACAACCAAGAAGATACAGTACCATTCTGTATGATATTGACATTGAAGATTTTCGATGATG
AGCTTATATACTATGACAACACAGCTAGGTTCCCAGCGAACGAATCAACTTCATTACTAAATCAAA
ACCAAAGAATCCCCATTATAGATCACTTAATTTGAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC
GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGATCGTGGCTCTAACAAAGATGGTACTGATA
ATGGAAACAACAGTGATCACAATATTAATTTCTCCTTTGACTGCTAATAATAATAATAAACGTCA
ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACAACATTGCTAATAATAGAG
CATTTCCATTTCCTTATCAAGATCAACAACATCAATTATTACTACGACTACGATGATTTTGACCAAG
AATCACAATCAATGGACCCAATTTTGATTTGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA
ATTTTAACAACAACAATAACCCCAAAAGATTTGGCGACAGTCATTTTTTTCTACCAAGAAAGACAG
ATCAGTATAGTCAAAGAACAAGCTTCTAAAGTCATGCATTTATACCTTTGTTTGTATATTAATTG
TGCTTACCATAGGGTTTGTATTGGGGTTTGTTTTGGCCACAACAAAAGATTTAACTGATGTAGGTA
TCACATCCATTGAGAACCCCATTTGTTAGTAAAGATGAGTTAGTTTTCATGTTGTTATTGAAGCAT
TTAATCCAGGGTGGTTTTCCTGTTGACATCAATGAAGTAGAGTTGGATTTATTTGCAAGAAGTGGCT
ATCTACCTGATACAGATAATCTGAAAAATATCTAACAATGAGGAGGGTCACAAAAGTAGAGACGGTTA
AATTAGGAACGATTTTGAATTTTGAATCGGTTCTCAATTTCAAAGGTGGGTTTCTCTCTCGAGAAC
CGACAATTCAAAGGGAGGAATCCGATTATTATATCCTGGCAAAAATGTTACTGCCGAGGCTAAAT
TGGTTGTAAATATGGCTGATATTAATAATAGCTGCTTCCAATAGCATTGCTAAAGAAAGCACTACTA
GTAATGACACCAACGATAATGACAACCTCAAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCTCAAGATCAGTCGTGGTTA
GAAAAACTGGGTATATTGATCCTACCTTATTCTGTAATACCACAAGGAGAGAATAATATTTCAATTT
AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDNDSNINNNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSLRSPSILE
GEQLQYFHDVPVRQQQFKLPSTKAPSISSNSSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQPQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKLR
STTSKLFDDKKGSQPRRYSTIPDDIDIEDFDELIYYDNTARFPANESTSLLNQNQRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTNGNNSDHNINSPLTANNNNNNVNHNHNDHGDNKKST
NNNNIANNRAFPFPYQDQQHYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFLATTKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPGWFSVDINEVELDLFARSGYLPDTONSKI SNMGGSQKVETVKLGITILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVVNMADIKIAASNSIAKESTTSNDTNDNDSKKW
EIISNPFDLIITGVLYDLFPSTRSRVVRKTGYIDPTLFVIPPQGENNISI

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;

CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTTACCAACCAAAACCTCTGATATCAATGATTGCAAAAGATTCATTCA
ACCCCGGTTAGCTGTTTGGAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC
AATACTTGTTTACCTTTTCATCTGATTCTAATTGGTTCATAGCAATATAGTCTCTTCTGTTGTTTGA
TATTAATATAAATAAAACCTTATTTATCAGCTGTTTGTAGTCTCGCAAATTTGAAACCATGGATG
AGTAAACTTGTGTGTAGATGAGCTCAAATATCTAGTGGGAACAATTGTGTAGTACTCTTTGATA
AATATCCAAGAACAGTCGTGCAAGTTTCAAATACCATCGCAAAAATCCTAACAAAAAATAAT

TAATAAAGAAAAGAAATAATTCTATAATAGCTCATCACAACAATTCGTCTACACTTCCCACCTGAT
TTGTTGGTTTAAATATAATAAGACAAACCTCAGAAGCTATGATAAGAAAACAGGCTAGAGAAAGAA
GAGAGTATCTTTATAGAAAAGGCTTTACAGCTTCAGGAATCTTCTTAAACAGAAAAAAGACAACAAT
TGAAAGCAGCTCTAGCAAGTGGAATAATCATTATCAAAGGAGCTTGCCGAAGATGAAAAATTACAAC
GTGATTTTATTTACGATGAAAAGTGAACAAATAGAAATTGATGACGAATACAGTCGGTTGTCGGGAA
TATCTGATCCAAAAGTTGTTATTACCACATCCCGTGATCCATCTGTCAAGTTGCTACAATTCCTGA
AAGAAATCAAGTTAATGTTTCCAAATAGCTTGAAGTTGAATCGAGGAAACTATATAATCTCAGATT
TGGTAAGTACCTGTAATAGAGTGCAAGTTTCCGATATGATTTTATTGCACGAGCATCGTGGTGTCC
CATCAAGTTTAACTGTAAGCCACTTTCCTCATGGCCCAACTGCGATTTTTCAGTTACATAATGTCA
AACTAAGACACGATTTGCCAAACTTGGGAAACGTCTCAGAGTCTATCCTCACTTAATATTTGAGA
ATTTCCAATCCGACTTGGGTAAGCGTGTGGTTAAAATATTGCAACATTTGTTTCTCCAGGTGTCA
AGAAAGATAGCTCCAGAGTAATAACATTTGTCAATAACGATGACTACATCGGTGAGACACCATG
TTTACGTCAAACTAAGGATTCAGTGGAGTTGAGTGAGATTGGCCACGTTTCGAAATGAGATTGT
ATGAAATCAGACTAGGATTACCTGACAACAAAGATGCTGATGTGCGAGTGGCAGATGAGAAGATTCA
TAAGAACAGCTAATAGAAAGAATTACTTGTA

YNL075W_homolog 283aa (SEQ ID NO 428)

MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKSLSKELAEDKLQDFIYDESEQIEI
DDEYSRLSGISDPKVVITTSRDPVSKLLQFSKEIKLMFPNSLKLNRGNIIISDLVSTCNRVQVSDM
ILLHEHRGVPSLTVSHFPHGPTAIFTLHNVKLRHDLPLNGNVSESYPHLIFENFQSDLGKRVVKI
LQHLFPFPGVKDSSRVITFVNNDYISVRHHVYVKTGDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWQMRRFIRTANRKNYL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058
(SEQ ID NO 429)

TCCTTTTGTTTTTATTTTTTGCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTCCTAGGAACAGGA
AAAATAAAAACGAATAAACAACCAACCCCAATCGGCATGCATCGGAATTCCTTCAGCCCAATTAC
TTTATTTTTTGCCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCTTTATA
TGCAGTCTATTTTATTTTTCTCTTTTTTTTTTGGCTGTGTGTAAGCTTTTTTTTTTTCGCAGGTG
TTGAAAAAAAATCATTTTTACAGTTTACATTTCTCTAACTGCAAAAAGCTCTCGTTTTTTTGTA
GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTTCTTTTGAATAGTCAACC
AACAGCAAATAGCCCAAGGATCAAGCTTTCATCATTAATCATGCTCCTCTAAGATCTATCAGAAAACC
CAACTGAATTAGAATTAAAAGTTGCTCAAGCTTTCGTTGATTGGAATCTCAAGCTGATTTAAAAG
CTGAATTGAGACCATTACAATTCAAATCTATCAAAGAAATTGATGTTAATGGAGGTAAAAAGCTT
TAGCTGTTTTCGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAAGTACTAGATTAAGTAGAG
AATTAGAAAAAAATTTCCAGATAGACATGTTGTCTTTTAGCTGAAAGAAGAATCTTACCAAAAC
CAGCTAGAAAAGCTAGAAAACAACAAAAAGACCAAGATCAAGAACTTTGACTGCTGTTTCATGATA
AAATTTTGGAAGATTTAGTTTTCCCAACTGAAATCATTGGTAAAAGAGTTAGATACTTGGTTGGTG
GTAACAAAATCCAAAAAGTCTTGTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT
CTTTCCAACAATTGTACTCAAATTTGACTGGTAAACAAGTTGTTTTTGAAATCCCAGGTGAATCTC
ATTAG

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)

MSSKILSENPTLELELKVAQAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVFLAERRILPKPARKARKQKRPRSRTLAVHDKILEDLVFPTEII
GKRVRYLVGGNKIQKVLDDSKDSTAVDYKLDLSFQQLYSKLTGKQVVFEPGESH

YNL178W_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS:
501..1253 (SEQ ID NO 431)

TGTTTTGTTTTTGCAATCAACATAATAGAAGACCAACAAATAATTTCTATTTTTTTTGACTCTCC
CGTAGTTTTACACTTCTAGCCTCTCTTGTAATATACACCTAATTGACAGTACCATTAGGACCCCA
TCTTATTGTTAAGGATAATACTTCTTCTTCTTCTTCTTCTTGTAAATCAAATTTGCAATAAATA
AAAAAAAACAAAAACAAAGCCGACAAAGTTTCCATAAATGACTTATTTTGTGTAACGCATTAC
GTGATCATAATTTTTTTAAATTCAAAACTGAACCAATTCCTGCATATTGAGGTTGAAAAAAA
AGAAAAAGAAAATTTTTTCAATCTTGTGTTGAGGAGAGAGAGGTGAAAAATTTTTCTCTCTCTTT

CTTTCTTTTCATTCTCATATACCATAAACTTAAACAACCTTCTTTTACTTTTTCTTTCTTTTCCTTT
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAATGGTTAACGCTATCTTATCTAAGAAAA
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTG
AACAAAGTTATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTGGAAGTTATTGTTAAAGCTT
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAATCCATGAATTAACTTTCAATTGATTGTTA
AAAGATTCAAATTTATCTCCAGAAGGTATTGCCATTTATGCTGAAAGAGTTGAAGAAAGAGGTTTAT
CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTATTGCTCTGGTTTACCAATTAGAAGAGCTG
CTTATGGTGTTTTAAGATTTGCTATGGGTGCCGGTGTCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAAATATGCTGATGGTTTTTATGATTCAATCTGGTCAAC
CACTAGAGATTTTCAATTGATATTGCCATTAGACATGTTTTAATGAGACAAGGTGTTTTGGGTATCA
AAGTTAAATTTATGAAGATCCAGCTGCTAATAGATTTGGTCCAAGAGCTTTACCAGATGCTGTGTTA
AAATTGCTGAAGCTAAAGATGAAGATGAAGTTATTCCAGCTCCAAGCTGTTAAATCTTATAAACAAA
CTGCTGAAGATGAACTGAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
AA

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLEQGRR
IHELTSLIVKRFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA
KGVEVVISGKLRAARAKSQKYADGFMIHSGQPTRDFIDIAIRHVLMRQGVLGKVKIMKDPANRF
GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAAGTGAACCTCAAATCACATTCTTCGGCATATATCAAACCATTTATTAGT
TTTATCACGTAAATCTTCAATATACTCAGCCACCCATTGATCATTGGTTCTTCTAGTAAGTAATAT
TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCACTGGTCCCACCAGT
AATCATAAACACTTTCCCATGCATGTCTCGCTCCACGTATTGGTGGCACCATTGGAAATAATACTT
GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCAGTGGCATAATTGGTATATC
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTTCAAAATTTGGTTGCCTTTTTATTCT
TCTTGTCTCTTTTTTTTTTTCAGTGCTAACATAATTTGGGATGTATGTATTGAAAAAATAATTTTG
TACAATTTCTTGTCTTGTCTTCCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG
TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCCAGGAGAAAGAAATTTTCACTGCTGTTCCCTAACAAAGGCATTAATCA
ATGTATATTTCATGGGGAAAAAGAAAGTGTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA
TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAAGTTATACA
AATTACCAAATTACCGAGTTCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTGTACATTT
GGGAATTAAGTTTCAGGCAATTTATTATGTGTCAGAGACGCCCATTTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTTAATTACTGGAGGAGAGGATGCCAGATGTCTTGTATGGAATT
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT
ATACAACCTTCAGAAGACAGCACGGTCAGGATTTATGATATAGTCACAAAAGAGTTTGTAAACCACAT
TTATTTTACCCAGTTCCGCTGAATGTATCACCAAGGATCCAGCTAATAGAGCGTTATATGTCGGGT
TGAATAACGGTCTTGTAAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTTGTGAAA
GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAATTTAAAAGAGACATTTGTTG
CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTACGAAATTGACAATTTCTT
TTGATGGTACAAGTATAATATCTGGTGATTCTGAAGGCAGAGTGTGTTGTCTGACATTGTAACGA
ACAAGTTGTGAAATCATTCACACCTTGTAACCTCTCCAATAGCTTATATTGCTGTTGAAACTATCC
CTGATGACTTTGTCAATAACTTAGCTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA
TGATACCTCAATTTAAACGAGTACTAGCAAGCACCATTCTGAAGAACATCAGATATCTTGGACA
TTCCTGGTAAACACCGCAACCACCAACGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG
GCAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAACTCTATTGTCAAACAAGTTG
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTA
GAAACAAACATGAAGAATTAATTAAAGAACATGCCAAATTTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVLVPLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIEALTCITLINHPNGSNNN
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAH YQGITTIIKGSSCGTFLITGG
EDARCLVWNLAELISIIDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSEDSTVRIYD
IVTKSLLTTFILPSSAECITKDPANRALYVGLNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA
DQNLKETFVAHQQKTKTGDDKPVVVTKLITISFDGTSIISGDSEGRV FVSDIVTKQVVKSF TPCNSP
IAYIAVETIPDDFVN NLATSTTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQKGQSEELQFKNLSGINSIVKQVGNENVS DLEERLQRV SQAYTEL RNKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAACTTTTTATATCCGAAAATTTTGGCCGGGAACGAAA
CGGCAAGAAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGTCTTCATCAGTTATAGCATTTCAATAA
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAATAAATCAATTGA
CACAGTCTTTTGAGATCTGTTATCTTGGCCTATAGCGTTT TAGGAAATTGCGGTATTTCTTGCTCT
GTTTTTCTTTTATCTATTTTCGCACGACTTGGGGTGGTTTGTGTGACTTTTTTAGCAAAATTAATTT
TGTCGGTCTTCGCAGTAAAAATAAAAAATCAAAAAA AAAAAACAAATTGACTTTTTTTTTTACTTTT
CTTCTTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCACTACTGTTGCCACTGTTT
TTGCTATTTCTCTCATTAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA
CCAAATATGTCACTGAAACTACCCACAGATACGGTCGTTT GACAAAACAGTAGATCTAAAAAGC
CAAAGGAAACTGGTACTCACAGATACGGTAAATTCAACAAGACTCCACGTCCAGTTACCACAAC TG
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
CTTCTTCCAACTCTACCACCTCTAGTGGTAACAATGGTGTGCGCCACTGGTGTGAGCTTGGGTCTTG
CTGGTGTCTTAGCTGTTGGTGCTGCTTTGGTCATCTAA

YNL190W_homolog 131aa (SEQ ID NO 436)

MKFTTVATVF AISSLAAAKGGEKDHGKASTVTKYVTETTHRYGRFDKTSRSKKPKETGTHRYGKFN
KTPRPVTTTTVLVKESDLPKKRDAVVARD SKNASSNSTSSGNGVATGVSLGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGTTTTTTTTTTTGGGTGGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG
TTTCGGTTCTACTTGTTCTTTTTTTTTTATCTCCTCGTTAATCCTAATTTTGTGTAACAAATTAAT
TATAGGGAGTTGGAATAATAAGCTTGAAAAGAAAGAAAGAAAGAAATACCAACGTGGAATTTCT
ATTACGTAAGTCACTATAACTTGCATAGAAATTTAGGTTTTCAATTTAAGAAAGATTAATCAAC
TGAATTAAGCAATTGAAACGAATTGAACCAGCTCAGCATTTATTTTTTCGTTTTCTTTTTTTTCAA
GGGGTGGGTGAAAGAAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTCTCTCTT
TCTCTCTCTAACTCAATTTCAATTTTTCCCAAACCAAATTTCTTTCTTTCTTTCTTTTATT
TTTTACTCAATTGAATCAATATTA AAAACAATAAAAGCCATGTCAGCTAACGATTTTATTCATCTG
GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCAATGATGAAC
AACAAGACAGAGGGTTATTATCTACTGTCGCCGGTGGTGTGCTGGTGGTTATGGTGGTCACAAAT
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAATATGGTG
GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT
ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
GTGGTGGTTACGGTGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTTGGCGGTGGCAGAC
CAGATGACCGTTTTGGTGGCGGTAGACCAGATGACCGTTTTGGAGGTGACAGAAGAGATGATAGAA
GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGT LGTV
LGAIGGAIGANKLEDAYEDRKEHKKEHQYQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRFGGDRRDDRRDDRRW

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTTGAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
TTTGAGGGGATGTTTCATTAGCAATGTATATAATTATTGTATATTATGACAAAAGAAAGAAAAAGAA
AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAATT
TGAAAGACAATCCGAATGTAGTGCTTGCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT
TGAGGAAAATTCAGATAGCTAACGGTTTTGCGATTACGAATTTTCGCAACCAAATAAATATGTGACA
AGGAATACACTACTGATCAAGGTTATTCTTAGTACAATGGAAAAAAGGAAGCAACAAAA
AAACGAGAAATTAATGAACACGACTTCACTTCTACAACCTACTGGGAAAAAAGGCAGAGAGTTA
TTGAAAAAGGATCATATCAAGTTCCTTATTGTATATTATATGAAGTTTTCTGTTTTAGTATTACTTG
CCAGTTACTTAGTTGGTGTGAATTTCTGATTGTTGATACTTCAGAGGAATTAATTTGTCCAGATC
CAGAAAACCCTTTAGATTGTTATCCAAAATTGTTTGTTCACAAACGAGTGGCAAACCATTAAC
CAGGTCAAGATATACCACCTGGGTTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG
ATCATTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA
AACAGGAGCAGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGACGCAGCTTGTC
TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAAGGTTGCATTTGGCACTAGATACTT
TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTTCAGA
GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGACTTGG
GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG
TGGATAATTTGTTTGAGCAATTAGCGAATGAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA
TTCAAGCTTTAGTCCAAAATAGCCATTTTGAAGACAATATTTTTCATTTGACCACAGTTCGGGGT
TAAATGATTTAATAGCGATTTTTCCTCAAACTTGGTCCAACTCAAAGTCCAGGGCAAGTAACATTT
TAGAGGATTTACAATTGTTCCAGTAACAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT
CACAGGTTTCAAATTTATTTCAGAAATTCCTTTGTTGGAAATAAACTTGACGAGAAGAATTTCAAGT
CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTCACTTTC
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAGAGACGATTATTCACAAG
AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT
TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASYLVGVNSSIIVDTSEELICPDPENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVRL
NIDTLEKEAKLMSADEKDEPVQEVVVGELQDHSREAITENLQKLHESKHPEVKQEHARTKVSQG
DLNFDAAACSEIESFKPHESDVERLHLALDTLEELSHDIEFGVKLTSDKAIFQSFVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNILTNFDKSYVDNLFQLANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFVPTNDRRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEEVESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADDEL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public: 28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTCCTTGATTTTAGAGCTGTTAATTATACCTTTTTTGTTCCTCAAATAAGCGCTAAAAA
TGATTGAAATTAATAATACTAATACTATTCAGGTCAAAGTAAACACTATAAAACAATATATTTCAAT
AACAGGAGCAGTAATTAGCTTCAACATCAAGGTACTCTTTTATTTTCTACCAAAAACACATCTGA
AGTAGCTCTTATCCATAGATCCAAATATTTTAACCTTTTTTTTCTACTCTCATCTACTTTTTT
TTGCAACACTTACTGCTCACAAACGCAATGACCATACCATTAAATTTCAATAATCAAAATCAAGAGCT
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAACAACACCGATTCTATTTTCACTAATAACAG
ACAGAAAGGGGTTGTACTATTTTGTAAACACATCCCACCGTTTGGCCCTTTTACATAACCATATTGA
TACCTCAATTGGTCCTTACACTAGTCATTTACCTGATTATGTTTTCATTGTTCTTCCACCTCAAG
CTATTGTATATACATTGTTAATGGGACCATTAGGGGTGATTGGTGCCTGGTATAGTTTGATCCTGC
AAGCGAGCACATTGTCTATATTTGTTGTCAATATCCTTAATGCCTCACATAACAGAGTGGCAT
ATGATGCAATATTGAGTAGAGAGTGTGCAATGATGTGGTACTAATGGGAAACTTAGGAGGTATA
GAAACTACCATTAGAGTAAGGGCCAGGAATACCTTAAGGCCATTCCAGATTTTTCGATCTTTC
CCTTCTCTTTGCTCAAGCTACTTGTGTTTTTTCGGTATTTACTTCATACCCTTTGTAGGTCCAATCA

TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
GGTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTTATGTTCCACCAATACTTTGG
GAGCTGCTTTGTGGGAGTTGATATTGAACAACAAGAGAAGGCCGTCACAGAGAATGTGGCCGCAG
CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
AACCAGCAACTAATATACCTGAGGCTACCCCAAAAAGTCTACAAATACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)

MFSLFFPPQAIIVYTLMLGPLGVIGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRACANDV
VLMGKLRIRYRKLPIRVRRAREYLKAIPDFSIFPFSLLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK
AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPFIMMFMFTNTLGAALWAVDIEQQE
KAVTENVAATTTATDNTSVNQQLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:
948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTGATTTTGTTTAACAGTGAA
AGTTTTTATTTTTTTTTTTTGTTTAAAGTTTTTATTTTTTTTTTTGTTTAAAGTTTTTGTATTATACAA
TATTTAAATTATAGTAATCATCCTATAAATTTCAAAGTCAAAGACAGATCTTAAAGTCTAATTTAA
TAACCTCTCTATGGCCTTCTGTGTCAAATTTGTTGTCGTTTGATAACAAGTTTGGAAACGGTAATGGTT
GAAATTAGAAAAGAAAAAAATTACACATGGTAGCAGCTGATGTATAGAACTTTCTAGCAAAAAAAA
AAAGAAAGAATTTTTTTTTTCTTCCATTTTTTCAAATTTGAGAGATCGAAATAATTTCTTGAATTTA
TTAAAGGGAACCCCTTCCCGAAAAATCCAAAACCAAACCTTCCACCCAAATATCAAATAACTAAC
TTATCATTTCCAACAGATAATATTTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
AAGGTAACAAATATTTTGCTGCTAAAGATTTTGAAGAGGCGATTGAAGCATTCACTAAAGCAATTG
AAGCATCACCTGAACCAAAACCATGTTCTTTATTCAAATCGTTCGGATCTTATGCCTCTTTAAAG
ATTTTAAACAACGCATTTAAAGATGCTCAAGAATGTGTCAGATCAATCCTAGTTGGGCCAAAGGGT
ATAATAGAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA
AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAATCAGTTGAATCTGCTT
TATCATCTGGTGGTGGTGGTATGACAAGGATTTAGGATTTGGTAAAATTTTAAATGATCCTAATCTTT
ATACTAAATTGAAAAATAATCCTAAAAACAAGTGAATTTATGAATGATCCTCAATTTGTTGCTAAAC
TTGAACGTCTTAAACTAATCCACAATTTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA
CGGCTTTTGTGCTTTAATGGGTATTGACATGGATTTACCAAATATGGGATTCAGTCTCCAAACG
AATCACAATCCAATGCATCAGAACCAAAACCTGGAACCAAAATCAGTACCAGAATCTAAACCAGAAC
CAAAAGCAGAACAAAAGGAAGAAGAATCAACCTCAGCCAAAAGATGAAGACACTCCAATGACTGATG
CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAAGCTGACAATGCTAAAGCTGAAGGTAATG
CCTTATACAAGAAACGTCAATTTGATGAAGCAATTGCCGCTTATAATAAGGCTTGGGAATTACATA
AGGATATCACTTATTTAAACAATCGTGCTGCTGCCGAATATGAAAAAGGTGATTATGATGCTGCTA
TTGCTACATGTGAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA
AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAAT
TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTTTAAATAAATTAAGATCAACTCAACGTG
AAATTTAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG
GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA
GAGCACCAGAAGATGCTAGAGGATATTCTAATCGTGCTGCTGCATTGGCAAATTTGTTATCATTTTC
CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTTCATTAGAGCTTATATTA
GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTCATGGATACTTTAACCGAGGCAA
GAATAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA
CTTATCAAAGATTTCAAGCCATTGAAGGTGAAACTCCTGAACAAACTATGGAAAGAGTTTCTAAAG
ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA
ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG
CTGCTGGTGTATTTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)

MTTAD EYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLVSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEFGLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGGDDKDLGF
GKILNDPNLYTKLKNPNKTSFEMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTFAALMGIDMDL
PNMGFTAPNESQSNASEPKSEPKSVPEKPEPKAEQKEEESTSAKDEDTPMTDAQDDTNDNDAKTO

ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYKGDYDAAIATCEKAIDEGRD
MRADYKLIAKSFARLGNIIYLKDELPEAVKNFEKSLTEHRTPDVLNKLIRSTQREIKTRELNAYIDP
EKAEEARLQKEYFTKGDWPNVAVKAYTEMIKRAPEDARGYSNRAAALAKLLSFPDAIQDCNKAIEK
DPNFIRAYIRKANAQLAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAIEGETP
EQTMERVSVDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKINMLIAAGVIRTR

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)

CCACTAACAACTTTTTTTTGAAGTATACACCACTGAAAAAAAAAAAAAAAAATTTTTGTAAAAAATCT
TAAGAATTTTCAGTTTAGAAGGTATTCAACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA
ATAGAATAAGAGCATGACAACAAGGGATACAAGCTTGAAAAAGAAAAAGGGTGGGATATCTTAA
AATTATTAAAGAGTTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTCGATTT
TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA
AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT
AATATGTCCTACCCCTTGTCAACTTGTCTATAAATTTATTGCTCGTCCTTTAAAAGAAATGAATAA
AAAGATTTACTAACTTAATTTCAATTATTTATAGAAAGATGTCTAGATTAAACGAATATCAAGTTA
TTGGTTCGTAATTTACCAACTGAATCCGTTCCAGAACCAGTTGTTTCAAGATGAGAATTTTTGCTC
CAACACCGTTGTTGCCAAATCAAGATATTGGTATTTCTTGCAAAAATTGCATAAAGTTAAAAAAG
CTTCTGGTGAAATGTATCTGTCAACATTTCTGGAAGCTAAACCAACTAAAGTTAAAACTTTTG
GTATTTGGTTAAGATATGAATCCAGATCTGGTATTCATAACATGTACAAAGAATACAGAGATGTTA
CTAGAGTTGGTGTCTGTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA
GTATCCATATTTTGAAAGTTGTTGAATTAGAAAAACTGATGATGTTAAAAGACAATACGTTAAAC
AATTTTTGACTAAAGATTTGAAATTTCCCATTAACACACAGAGTCCAAAAATCTAAGAAATTGTTCC
AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)

MSRLNEYQVIGRNLPTESVPEPKLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE
AKPTKVKTFGIWLRYESRSGIHMYKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT
DDVKRQYVKQFLTKDLKFPLPHRVQKSKLFFQATAPTTFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS:
501..929 (SEQ ID NO 447)

TGTTTACTTTTTCTGTAGTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTTCATTAACAACAATA
TTAACATACCTTTGTCACAAGCAATTATATTGAAGTTTTTTTGATACAAGTGTGTTGTTTTTTGTG
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAGAAAAATTACGAAGTAGA
AATATTGGTAGCGCGTTAGGGCTATAGCCCTATTTAGTTTGTGCACCACACGACTTACAATTTTTT
TTTTTTTCTTTCTTAGAATCCTTGAGGCACTGACACTGTACTCTCTCTCTCTCTCTCTCTCTCG
TAGGTAGTGA AAAATTTCCACTAGTCTTCCCATAAACCCACCTAGGTTCTTTCTTTTGGAACCACT
GAGCAGTAAATCAATTTACTTGACGAAGAAGTCTATACATAAATATAAACTTGTCCCTTCCCCC
CTTTTTTTTTTAACCTAAGAAAGAAAAAATTAAAAAATGTCTGACGTTGAACAAGAACAATTTG
TTGAAGAAGTTGTTGTTGAAGAACAATCCGGTGCCATCACCATTGAAGATGCTTTAAAAGTTGTTT
TAAGAACTTCTTTAGTCCATGATGGTTTAGCTAGAGGTTTAAAGAGAAGCTTCTAAAGCTTTATCTA
AAAGAGAAGCTCAATTATGTGTTTTGTGTGACTCTGTTACTGAAGAATCAATCATCAAATTGGTTG
AAGCTTTATGTAATGAACCAGAAGAAAAAATCCCATTGATTAAAGTTTCCGATGCTAAATTATTGG
GTGAATGGGCTGGTTTATGTCAATTAGATAGAGATGGTAATGCTAGAAAAGTTGTTGGTGCCTCTT
GTGTTGTTGTCAAAAACCTGGGGTGCTGATTCTGATGAAAGAAACATCTTGTGGAACACTTTTCTC
ACAATAA

YOR369C_homolog 143aa (SEQ ID NO 448)

MSDVEQEIVVEEVVVEEQSGAITIEDALKVVLRTSLVHDGLARGLREASKALSKREAQLCVLCDSV
TEESIIKLVEALCNEPEEKIPLIKVSDAKLLGEWAGLCQLDRDGNARKVVGASCVVVKNWGADSDE
RNILLEHFSQQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS:
501..878 (SEQ ID NO 449)

AAAATTTCCAATCTTGAATTTTCATCTTCAACGTCATAAACTTGTCTGTTTGAATTTATCGTCCT
CATTATCGTTGTCAATTTTCATTGTCAATATTACGGTTACGATTTTGTCTTCCCTTTGAAG
TCTTTGACTCTAGCTGTTTCATCTGTCAATTACCCTTGGCTTGGTTTGTCTTACTGTTGAGCGATGAG
ACAAACTTTTTGATTGATTGCAACTGAAACAAAAAATACGACAGACACACACACACACAC
ACACAATTTTCAGCTCCTTCCAAGTCGTGTTTTTTTGGAAAGAAAAAACAACCTTGGCCCTAAA
AACTCTATGCTCTAACCGACAACATTAGATTACTTTGATAACTCACAACCTTTAATTAACACTATC
TACAAAATATGACAAGTACACCAATAACGTACAAGACACTAGTATGAAAGGCAAGCACAACTTGC
AAACAAAAAACCCTAACTTTTATTATAGTTTTGTTTGTATGTTATTTTGTCTTATACTAACTAAAA
TCTGTTTTTTTTTTTTTTTCAAAGGCCGATTCCTATATTTAATGATCTAATCAACAATATCATTAAC
AACATACATTAACAGTTTAACCAATATTAAGATCATTCCTCATTATTAATTCATCTAATAGCA
ATACTAATAGCAATACCAACGGTACAATTGCCAGTAATGGTGGAAATGGGACTACAAGTGATGAAA
ATAATGAAATTGAAAATTCAACAATTCAAGATAAATCAAAATTAAACAATTAGAACTTCAAGGT
ATTTCCGATGTCTTAATTGTGGTAGAAAATATTGCCGGTGGAAAGATTTGCATCTCATATAAGTAAGT
GTTTAGAACGGAAACGGAAATGA

YPL047W_homolog 126aa (SEQ ID NO 450)

MLFCFILTKICFFFFSKADSIFNDLINNIKQHTLTSLTNIKDHSSLLNSSNSNTNSNTNGTIAN
GGNGTTSDENNEIENSTIQDKSKLKQLETSRYFRCLNCGRNIAGGRFASHISKLERKRK

YPL137C_homolog 5344bp public: 1..3342, PathoSeq: 3343..5344; CDS:
1250..5341 (SEQ ID NO 451)

CTCTAGAAGTAGGACATCGTATAGTGTATAAACACTCAATAAGTAATGAAGAAACACGTTTTGTG
TGCAATGTTAGCTGGCGAGCTCAATATTGGGTCTCTCCGCCGTCTGTCTGCCTTGCATTCTACTTT
TTTTCTCCTTATGGAACATTAGTACTAGTAGTGGTGGTAGTAGTTGCTGTTGTTGCACTTTGC
ACGTAGTTGTTTTCCCTCATCTTTTCATCTGATTATTCTGTCTTTGTTAACTGCATACAAAGGGA
GGGAAGAAGAAACAACAAAAGGGGAATTTGAATATACGTCAATCTTTAATCCTACTACCACGGG
GGGGGGGGGGTGCATCTTCTTGGTGTAATAATATGATGGAGATTGAGGTTATTAGACTTTTAGAA
AGAGGTCTTGGTTGAGTAAGGCGGGATAGCACAAATAATGCGTGTCTAATTGGTGCAGAGAATAATA
TGCTTTGGGGAACAATAGAAAGATGTAGCGAGAGAAATAGAATTNCAAGGGTAAGGATGATTAAC
TTTTTTTTTTTTTAATGCTTGGAGTACTTTGTTGTTGGAAAGAGTATTGCAGAAGTAATAGTTTAA
AAAAGAAAAGTATATACTTTAGTAATCGGAGAACAATTGAAATCAATATTTTGAAAAATATAGTTT
TATAGAGTAACCTGGGTCGAGGTGAACCCGAATTCAATATTGGTTTTCGGTTGTTATATGCTACAT
AACCATCCTCATCTTGAATGAACAAGGATAATAGAAATGAGTATATTAACAACAACATTATGT
TGTTACTGTTGTATTCTGTTTTTTGGTCAATTGCCATGGTAATTTTCATATTTAGTAACAATTTAGT
TTCATCGTAAGTCTCTCCTTCTCTGGGAGATGTTCTCTCTCTCTTTCTCTCTCTTGTGTTGTTGT
TGTTAATTGTTAATTGTTGATTATTGATTGTTCCCAATTAATAATCCGATAAACTTGAACAATAA
ATTGTCATCATAAATTTTTTTTTTAGAAAACTCACTCCATAAATTAATTTATTTATATATTAATTT
TAAATCGGAACCTCCGTCAATTGGATTCCGGTTTTTTTTTTTTTTTATTTGTTTCATTTATTTCTTGAT
TTTATTTTCTTTTTTGCTTCTACTTCTCTTTTATTTTCTTTAGTTTCATAATTTTTGACAGATAATA
CTTGAAACTGGTTAATTTTAAATCAACTTCGTGATTTTTTTCCGGAATCTAATAATATCAATGAC
CAGTAATCTGCCACCACCTGGTTCACAACTAACGATCAGAGACTACCCCAAAGCGGAGTTTCATC
CATACCCACAAATAAATTGCCTTTACCTAATGCCAATGAAGATTTTGCCACGGGTGTGTCGAATGG
AGATGTTGACTGGCTATTTTCGAGGTAAATCAAAGAAATTGGGGAAGAGATGGCTAACAACAATGC
CAATAAGGATGAACGAAAGAATAGTCATGGTAACATCAAAAACCTCGGAAAAAATACCGCAAAACC
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AGCTGAAGATGCTCAACGCCGAGCAATTATTGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA
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GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAATGAGTTGATTACTGCTGGACCAATTTT
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TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)

MTSNSPPLGSTTNDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNGDWDWLFGRGKSKKLGGKMMANN
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SSSASSKQPQSHSSSTPSTTTNGGGNSSAPKSSHSPKFNPSLVGPVSKHNREEDLVSLTNTL
PAGSGIPIKRKPSISGNSIFKDSFLDDASSPSSSLNSDGLKFFRRRSSVASTPSTHASTPRVIL
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MGYNIAMVTDFFYPQGGVEFHVYHLSQKLIELGHSVVIITHNYSSRNGVRVLTNGLKVYYVPLWV
IYRSSVFPTVFSCPFILRNIFIRENIEIIHGHGSFSTLCHAILHGRTMGLKTVFTDHSFLGFAEI
GSIMGNKALKFTFSDVGHVICVSHTCKENTVLRGSIDPIKVSVINAVISKDFKPKSHCVNKNYTK
EITIVVITRLFPNKGADLLTAVIPKICQLKPKVKFLIAGDGPKFLDLEQMREKYFLQERVTLVGAI
KHEEVRDVMVQGDIDYHLSLTEAFGTIVIEAASCLGYVTTKVGGIPEVLPNEMTSFAEPEENSLI
DAADIAINKIESNEIDYTSKFHDVAKMYSWNDIARRTENVNSLDLKLNESLHLRLQRYCCGII
AGKLYALCVIVDIFIFVILEWLYPADHIDKATKWPSAIKEEDESEETFIFFPNKVN

YPL218W_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455)
GATACAATTCACGACCTCTAATTTTCCTTAGTGATAGGTTAATCATGAAATATATAAAATGCTTAGA
AATAATTGAATAATGATATAAATATAATGTTGTGAAACTTGTGGAAAAATTTGACAGCCTAGTAAC
TCAAGTGTGTGTTACACTCTTGTATTATTATTATTATATCGTTTACAAGTAGATTTCTCATTTTGA
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CATTTACACGTACACCCTTAACTTGAAGGAAAAAACAACAAGAGAGACAAAGAAAGAGACAAA
GAAAATACTTTCAACAACGAAAGATTGAGATATTGGTGATTTTCACAAACCAAAAAAAGAATAC
ACAACCTTGATAGATTACAGAATTTGAACATTTCTAGAGTTTCTTATATTCCCCCAAGGTGGACAA
TTAATAATAACATTTGATTATACAAGAACATTTCAATCATGTGGATTTTGGACTGGTGTATGTAAT
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CACTTAATTATTTACAGTTCAAGATATATTATCATCATTAGGATTATGGAATAAACATGCCAAATT
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TACTTTTGATTTAGGTGGACATCAACAAGCTAGAAGATTATGGAAAGATTATTTCCCTGAAGTCAA
TGGTATTGTCTTTTGTAGTCGATGCTGATACCCGAAAGATTGCTGAATCCAAAGCTGAATTGGA
AAGTTTATTTAGAATTGAAGAATTGAGTCAAGTTCCATTTGTTATTTTGGGTAATAAGATTGATGT
TCCTACTGCAGTAGGGGAAATGGAATTGAAAAATGCCCTTGGATTATATAATACTACTGGTAAAGA
TACTGGTAAATTGCCTGAAGGTACTAGACCAATTGAAGTGTATGTTTCCGTTGTTATGAGATC
TGGATATGGTGAAGCCTTCAAATGGTTATCACAATACATTTAA

YPL218W_homolog 190aa (SEQ ID NO 456)
MWIFDWVQDILSSLGLWNKHAKLLFLGLDNAGKTTLLHMLKNDRLATLQPTLHPTSEELAIGSVRF
TTFDLGGHQQARRLWKDYFPEVNGIVFLVDAADTERFAESKAELESFRIEELSQVPFVILGNKID
VPTAVGEMELKNALGLYNTTGKDTGKLPEGTRPIEVFMVSVVMRSGYGEAFKWL SQYI

YOL127W_homolog 429 bp, public: 1..429, CDS: <1..429 (SEQ ID NO 475)
CTTATAGCAACTACTAAAGCTTCAGCTGCTAAAAAAGCTGCTTTGAAAGGTGTTAACGGTAAAAAG
GCTTTAAAAGTTAGAACTAGTACTACTTTTCAGATTACCAAAAACCTTAAAAATTAACGATCTCCA
AAATACCAAAGAAAATCAGTCCCACACTACAACAGATTGGATGCCACAAAATCATTTGTTGCTCCA
ATTGCCACTGAACTGCTATGAAAAAGTCAAGATGGTAACACTTTGGTTTTCCTAAGTTGACATC
AAATCCAACAAACACCAAATCAAATCTGCTGTTAAAGAATTATACGATGTTGATGCCTTATACGTT
AACACTTTGATCAGACCTAACGGTACCAAGAAAGCTTACATCAGATTAACCTCTGACTACGATGCT
TTGGATATTGCTAACAGAATCGGTTACATCTAA

YOL127W_homolog 142 aa (SEQ ID NO 476)
LIATTKASAAKKAALKGVNGKKALKVRTSTTFRLPKTLKLRSPKYQRKSVPHYNRLDAHKIIIVAP
IATETAMKKVEDGNTLVFQVDIKSNKHQIKSAVKELYDVDALYVNTLIRPNGTKKAYIRLTSYDA
LDIANRIGYI

YJL188C_homolog 117 bp public: 1..117, CDS: <1..>117 (SEQ ID NO 477)
TTAGATACCCAACTTAGTTCTTCTCCAGTGTCTTCTTTTAGCATTGTATCTGATTTTGTGTGTCAGT
TCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTTTGAGCCTTAGC

YJL188C_homolog 39 aa (SEQ ID NO 478)
LDTQLSSSPVSSFSIVSDFVSSQSDPLWQWSVLLLSLS

YGR183C_homolog 198 bp public: 1..198, CDS: 1..198 (SEQ ID NO 479)
ATGTTGACAGTCCTTGGTCGTTTACTTGAAAGAACTCAATCTACGTTGCCACTATCTTTGGCGGT
GCTTTTGTCTTTCCAAGGTTTTTTCGATGTTGCAGTGAACAAATGGTGGGAGGAACACAACAAAGCT
AAATTATGGA AAAACGTCAAAGGAAAATTCCTTGAAGGTGAAGGTGAAGAAGAAGATGACGAATAA

YGR183C_homolog 65 aa (SEQ ID NO 480)

MLTVLGRLLERNISIYVATIFGGAFQGFDDVAVNKKWEEHNKAKLWKNVKGKFLEGE GEEEDDE*

YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)

ATGGTTCAATCTATGACATCTGTCGTTAAGGCAGCTAATTTTCATTTTAGCAAGACCAACATTATCA
AAAATCATTACACCACTTGCTCAAAAATTCAGTCTTATGCAGGGTATAGAGAAATGGGATTAAAA
TTCAATGATTTACTTCTTGAAGAAACCCCAATTATGCAAACTGCTATTAAAAGATTACCTTCAGAA
TTAAATTATTCAAGAAATTTTAGAATTCTTACTGCTCATCAATTAGCTTTATCTCATCAATTATTA
CCAGCTGAAAAAGCTGTTAAACCTGAAGAAGATGATAATTATTTGATTCCTTATATTTTAGAAGCT
GAAAAGGAAGCTTTTTGAAAAAGCTGTATTGGGGAATATTGACGCTAGTGGGATTGTAATTAATACG
ACGAATAAGAAACGGACGAGGAAGAGGAAGAAGATGAGAAGGTCAAACATTGAAATATGAA

YDR529C_homolog 151 aa (SEQ ID NO 482)

MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLLEETPIMQTAIKRLPSE
LNYSRNFRILTAHQ LALSHQLLPAEKAVKPEEDDNYLIPYILEAEKEAFEKAVLGNIDASAIVINT
TNKKRTRKRKKMRRSNIEI

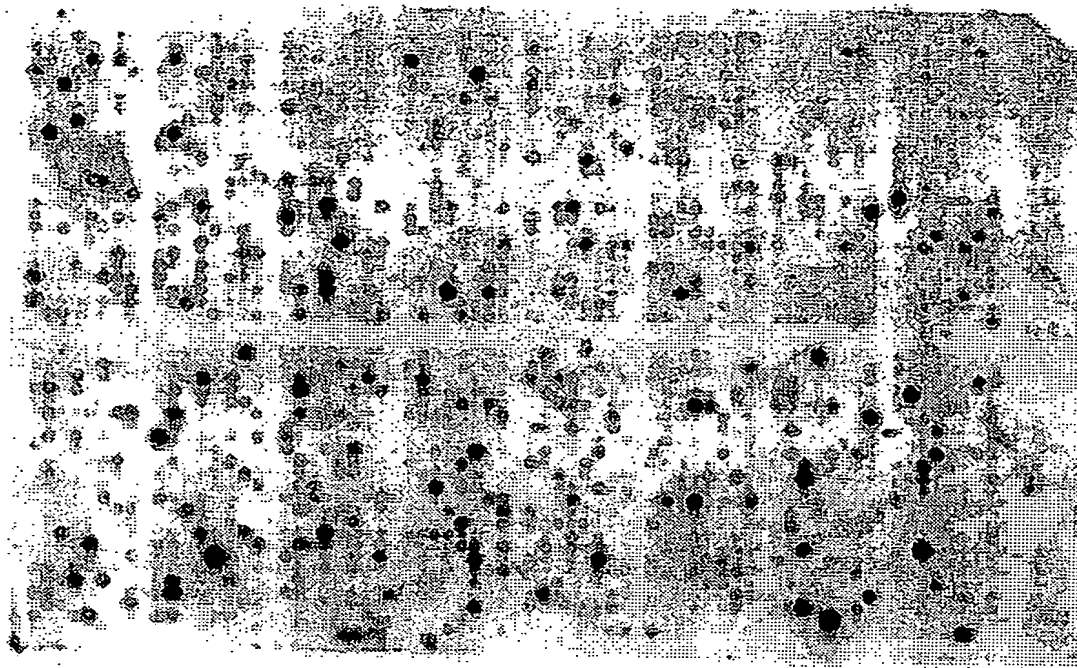
YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)

CTACAATTCTTGAGAAGCCTTAACACCACCTTTACCTGATTTCTTTGGCAACAAGTTTTGATGGAT
GTTTGGTAACACACCACCTTGGGCGATGGTGACATCACCAACAATTTGTTTAATTCTTCATCATTT
TCTGATGGCCAATTGTAAGTGTCTTGGGATTATTCTGGATTTCTTGTTGTCTCTGGCAGCGTTACC
AGCTAATTCCAAAATTTTCAGCAGCTAAATATTCCAAGACTGAAGTCAAGTACACTGGAGCACCAGA
ACCGATTCTCTGAGCGTAGTTACCTTTTCTTAACAATCTGTGGACTCTACCGACTGGGAAAGTCAA
ACCAGCTTTGGCTGATCTTGAAGTTGAAGCTTTTTCGGAAGTTCCTGCTTTACCTTTACCACCTGA
CAT

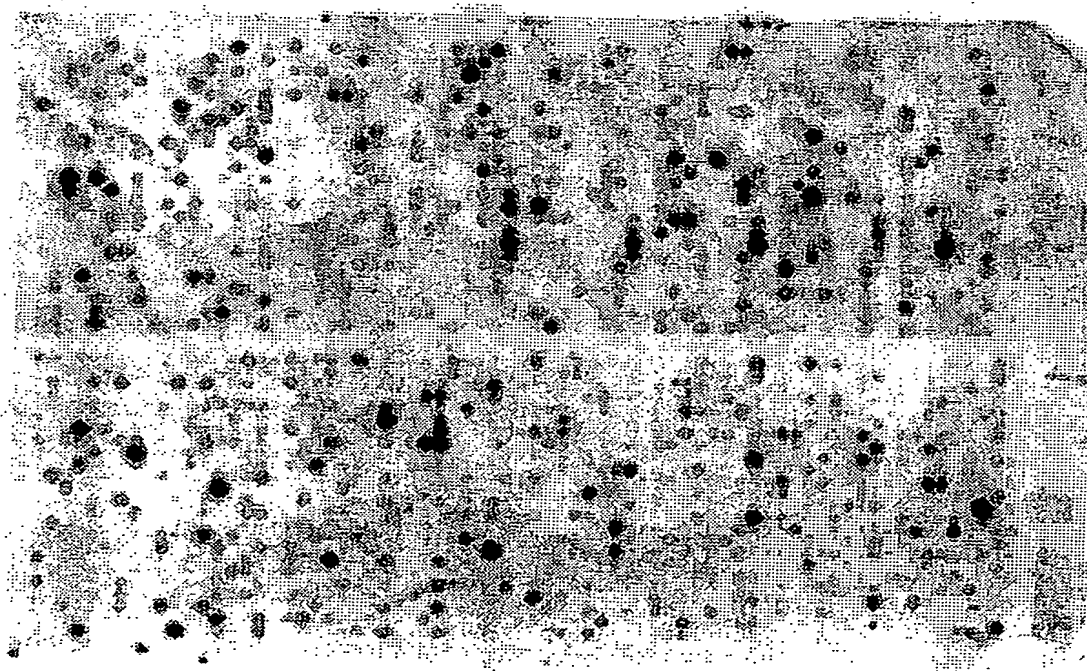
YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484)

MSGGKGKAGTSEKASTSRSAKAGLTFPVGRVHRLLRKGNYAQRIGSGAPVYLTSVLEYLAAEILEL
AGNAARDNKKSRRIIPRHLQLAIRNDEELNKLLGDVTIAQGGVLPNIHQNLPPKSGKGGVKASQEL

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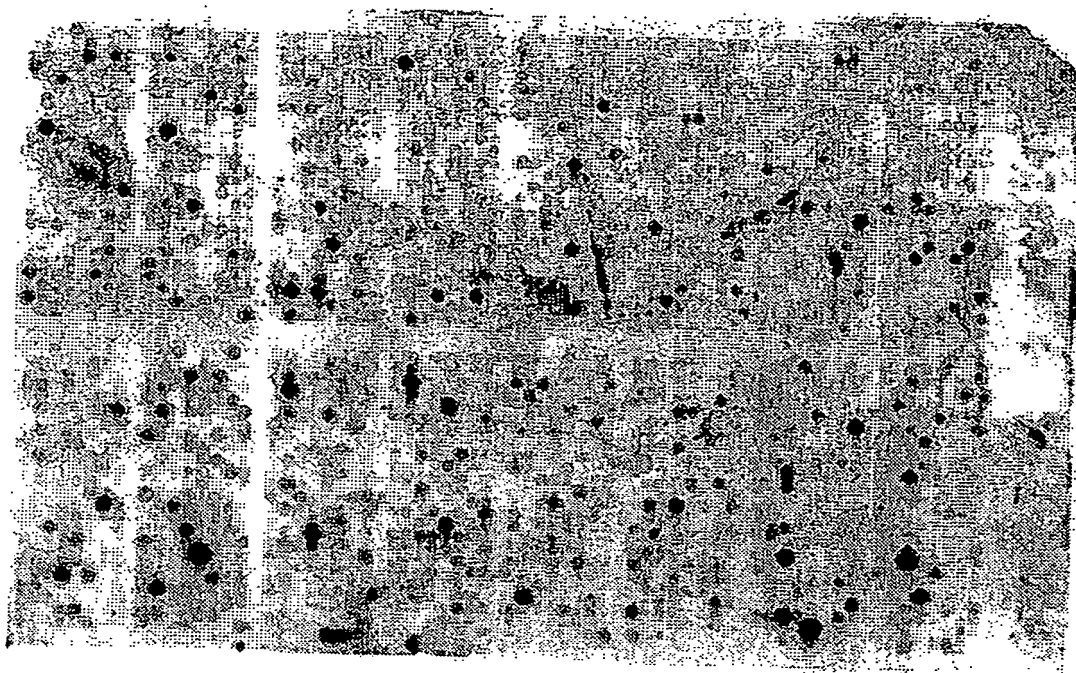
Filter I



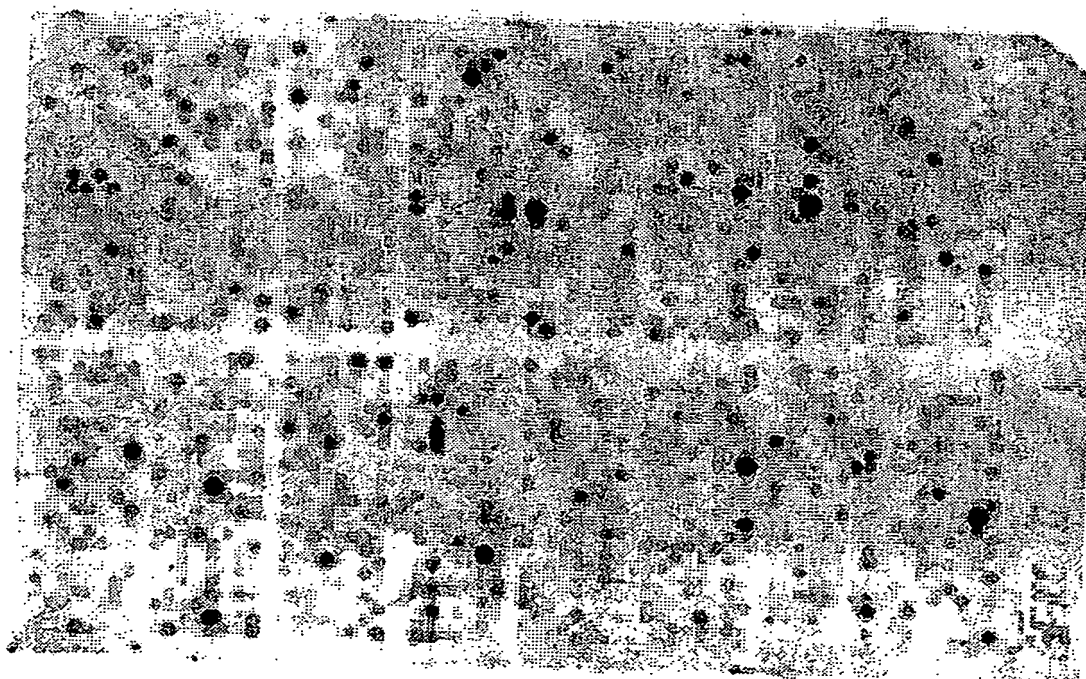
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FIG. 3A

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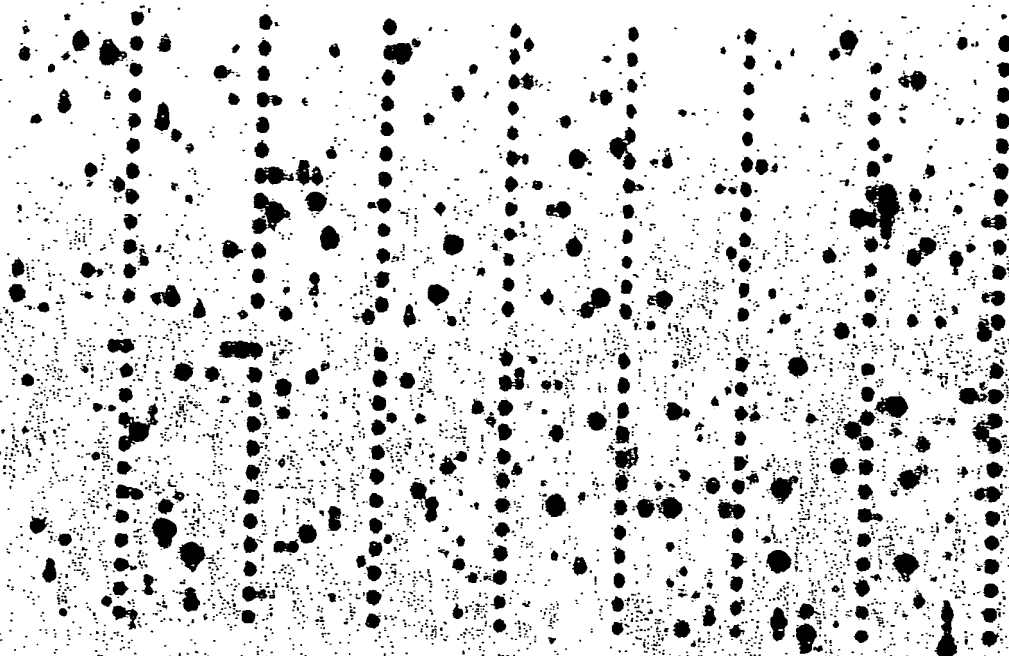
Filter I



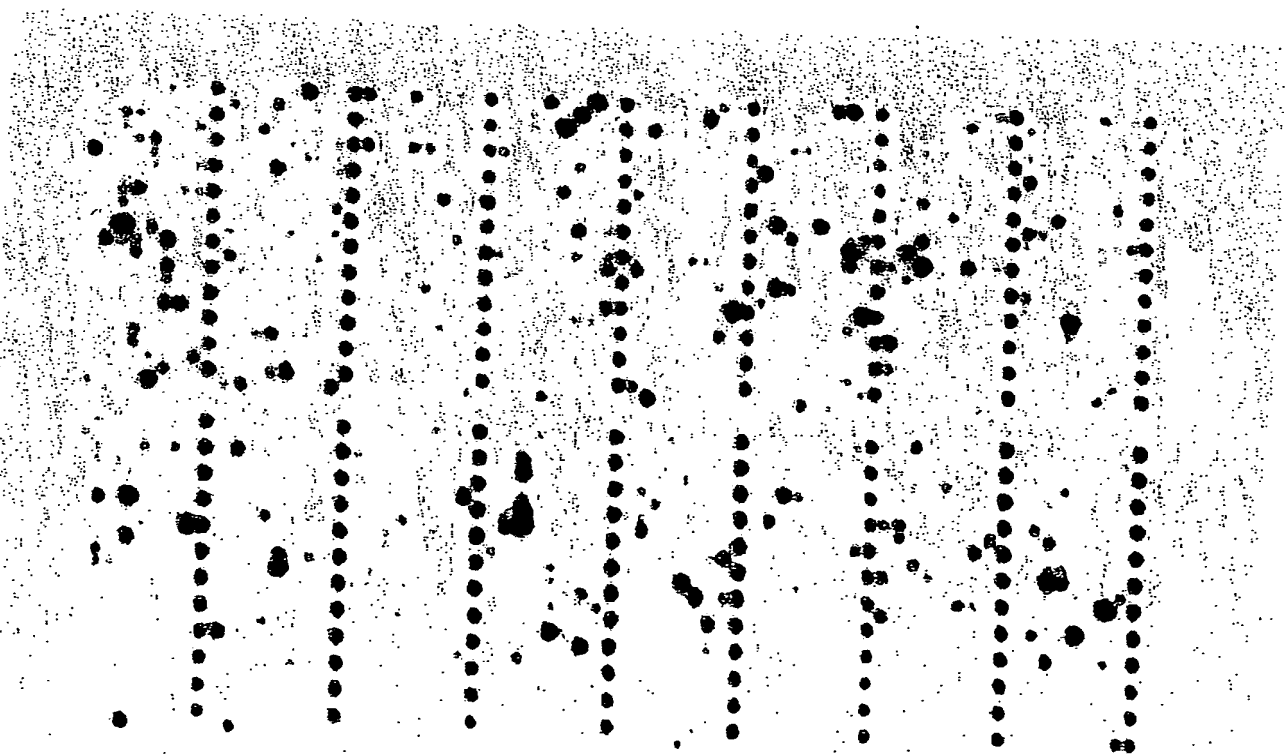
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FIG. 3B

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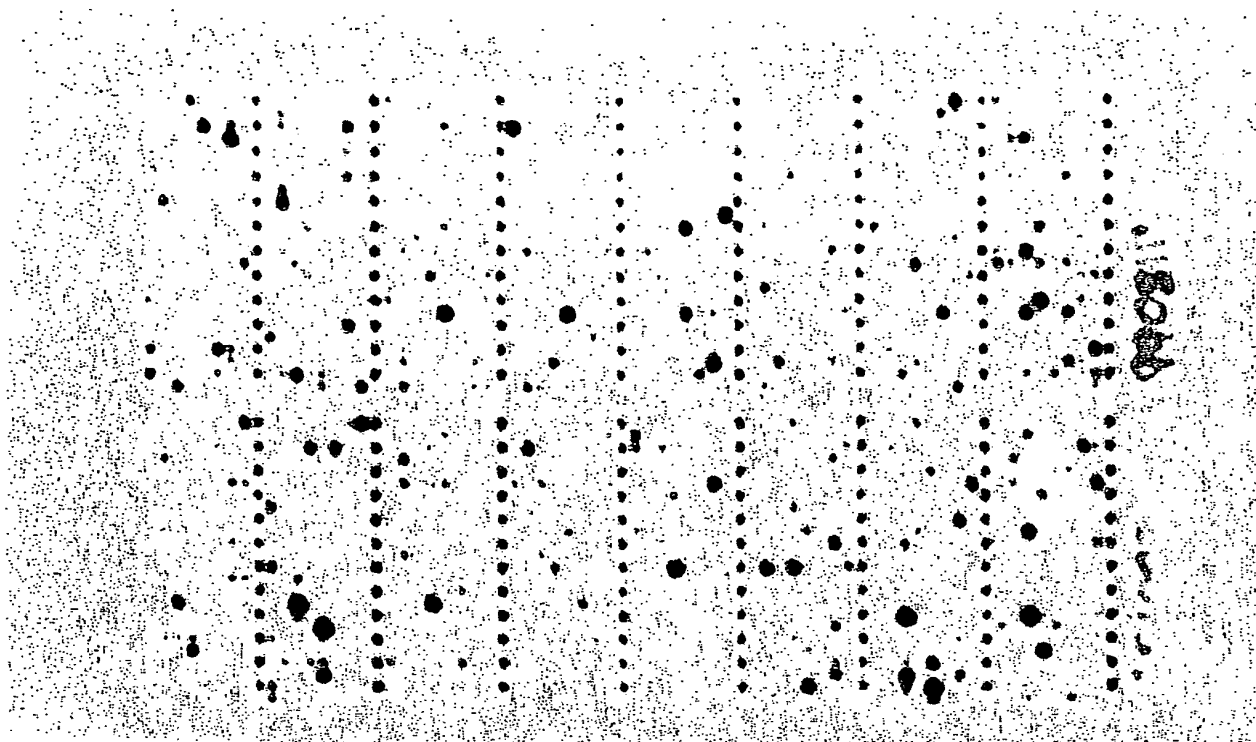
Filter I



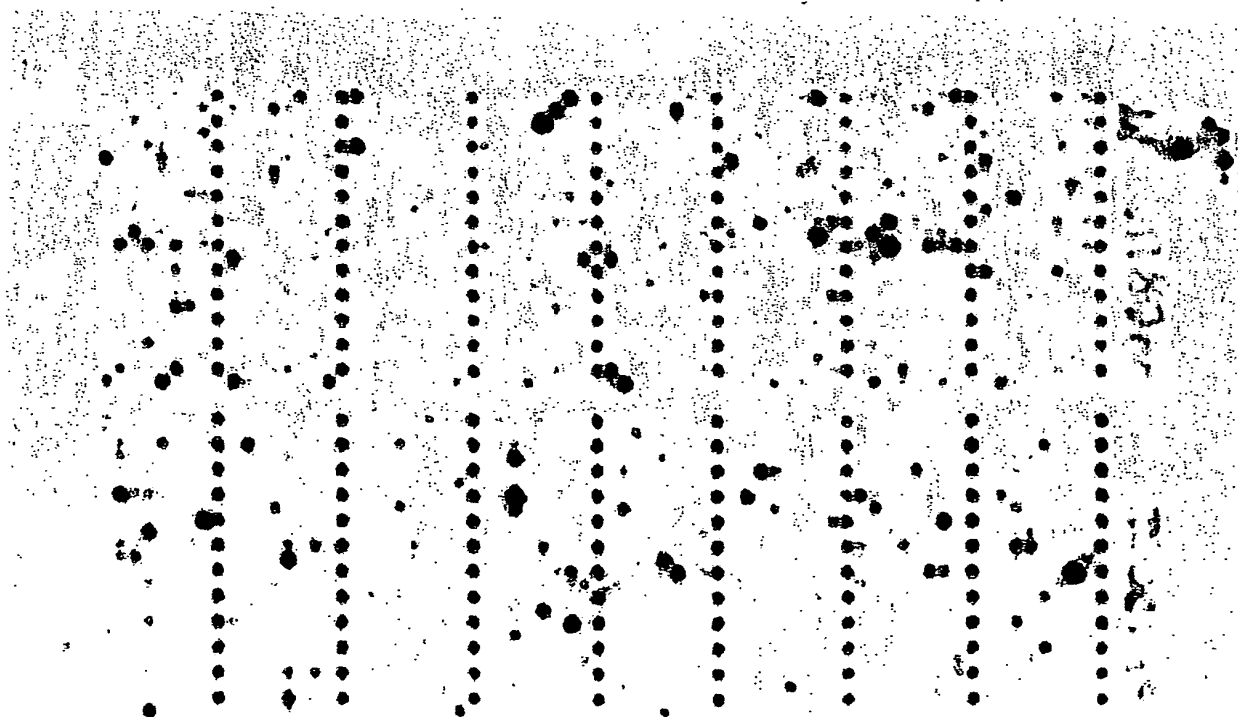
Filter II

FIG. 4A

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Filter I



Filter II

FIG. 4B